

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number

TO: Jegatheesan Seharaseyon

Art Unit: 1647

Location: REM-4C61/4C70 Serial Number: 09/658677

Thursday, July 07, 2005

From: Beverly Shears

Location: Biotech-Chem Library

REM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Sealen Noices

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.



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Sent: To: Subject:

Seharaseyon, Jegatheesan Thursday, June 30, 2005 9:27 AM STIC-Biotech/ChemLib RE:09/658677

Hi,

Please search SEQ ID NO: 2, 15 and 18 of 09/658,677 in the interference and commerical databases.

Thanks. Seyon

J.Seharaseyon Art Unit 1647 Remsen 4C61 Mailbox 4C70 Phone: (571)-272-0892 Fax: (571)-273-0892

TAFF USE ONLY	**************************************	**************************** Vendors and cost where applicable
earcher:earcher Phone: 2- Date Searcher Picked up: Date Completed: Date Completed: Date Time: Date Time:	NA#: AA#: Interference: SPDI: S/L: Oligomer: Encode/Transl: Text: Inventor: Litigation:	STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM: WWW/Internet: Other(Specify):

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ALIGNMENTS

Human Zsig13 variant #1, SEQ ID NO:2. AAB48972 standard; protein; 392 AA

Human Zsigl3; serine protease; chromosome 11q22.1; elastase homologue; glutamyl endopeptidase homologue; factor X homologue; trypsino homologue; trypsinogen homologue; protease homologue; collagenase homologue; protein degradation; food processing; brewing; alcohol production; laundry detergent component.

97US-0044185P. 98US-00062142.

New isolated serine protease (designated Zsigl3), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications (e.g. brewing).

Claim 1; Col 25-28; 26pp; English.

The invention relates to human Zsig13 proteins (AAB48972-B48974), and to DNA encoding them (AAC91782-C91784). The invention also relates to expression vectors and host cells comprising a human Zsig13 DNA, and the recombinant production of a human Zsig13 protein or its precursor. Zsig13 is a serine protease, and has significant homology to Bacillus licheniformis glutamyl endopeptidase, human clotting factor X, human elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine

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trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial processes to degrade unwanted proteins or alter the characteristics of
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                                                protein-containing compositions. It may also be used in industrial applications in which proteases are utilised, including food processing, brewing and alcohol production, and as a component of a laundry detergent. The present sequence represents a human Zsigl3 variant
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                                                                            New isolated serine protease (designated Zsigl3), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications
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AAY08657

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stimulation/suppression, haematopoiesis regulatory, tissue growth, cativithibin, chemostatic/themohic, haemostatic/thrombolytic, receptor/lidand, tumour inhibitor, anti-inflammatory and other undefined activities. The cDNAs can be utilized as probes for gene diagnosis and as gene sources for gene therapy. The CDNAs can also be used for large scale expression of proteins. The transformed cells can be used for detection of the corresponding ligands and for screening of novel low-molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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inflammatories, immune stimulators/suppressors and tissue growth
                  haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
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regulatory tissue growth; inhibin; chemostatic; chemokinetic;
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Pred. No. 1.1e-141;
1; Mismatches 5;
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Best Local Similarity 98.4%;
Matches 377; Conservative
                                  gene therapy; screening
                                                                                                                                                                                                                                                                 (PROT-) PROTEGENE INC
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                                                                   Homo sapiens
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                                                                                                                              Transmembrane domain; human; nutrition; cytokine; cell differentiation; immune stimulareseation; haemacopolesis; activin; regulatory tissue growth; inhibin; chemostatic; chemokinetic; haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the corresponding ligands and for screening of novel low-molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                               Human transmembrane domain containing protein from clone HP10493
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inflammatories, immune stimulators/suppressors and tissue growth
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Pred. No. 1.1e-141;
1; Migmatches 5;
AAY08657 standard; protein; 383 AA.
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98.4%;
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Best Local Similarity
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181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
      29-0CT-1997;
29-0CT-1997;
29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
03-NOV-1997;
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17-NOV-1997;
18-NOV-1997;
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        IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                             360
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                                                                                                                                                                                                                    Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                             TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                              IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                             Secreted protein; transmembrane protein; human; enterocolitis;
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                                                                                                    ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                               AAY13390 standard; protein; 383 AA
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97US-0059113P.
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24-0CT-1997;
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24-0CT-1997;
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17-OCT-1997;
17-OCT-1997;
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AAY13344-403 represent secreted and transmembrane human proteins. The CDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, collinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), poent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, Alzheimer's disease, Alzheimer's scarcing. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO265 can be used as a target for anti-tumor drugs. PRO263 can be used as a target for anti-tumor drugs. PRO269 can be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may be used as an anti-thrombotic agent; PRO287 polypeptides and portions may be used for treating problems of the kidney, uterus, endometrium, can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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9705-00637359-
9705-00637389-
9705-00642159-
9705-00642089-
9705-00642089-
9705-00651869-
9705-00651869-
9705-00651869-
9705-00661209-
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97US-0066840P
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Matches 377; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 acids in a sample and therefore identify or diagnose diseases associated at mappropriate TANGO expression of inactive polypeptides are cording to the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides or the according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a sensoriated with inappropriate TANGO expression by supplementing a sensoriate own production of the polypeptide of to rectify mutations that may respect the may also be used to identify and produce agonists and activity which may be used to modulate TANGO related processes and diseases. The polypeptides are
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                                                             300
                                                                                    301 TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                  Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein
                                                 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                                                                                     TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185;
TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine;
Becreted protein; transmembrane protein; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                       AAY88277 standard; protein; 383 AA
                                                                                                                                                     361 ITPLKYAQICYWIKGNYLDCREG
                                                                                                                                    361 ITPLKYAQICYWIKGNYLDCREG
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                                                                                                                                                                                                                                                                                                                                                             diagnosis; treatment; detection
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98US-00164169
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                                                                                                                                                                                                                                                                        16-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                             Human TANGO 186 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-293144/25
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                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
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particularly useful for use as antigens for producing antibodies to TANGO proteins which may be used for inhibiting the activity of TANGO proteins. They may also be used to detect and quantify the presence of TANGO proteins in samples and therefore identify patients in whom the protein is over- or under-expressed. This sequence represents the human TANGO 186 protein described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
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                                                                                                                                                                                                                                  Length 383;
                                                                                                                                                                                                                                                                                        Indele
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                                                                                                                                                                                                                                     Score 2044; DB 3;
Pred. No. 1.1e-141;
1; Mismatches 5;
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98US-0094983P.
98US-0102686P.
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                                                                                                                                                                                                                                     96.8%;
98.4%;
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Best Local Similarity 98.44
Matches 377; Conservative
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                                                                                                                                                                                    Sequence 383 AA;
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31-JUL-1998;
01-OCT-1998;
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Autorian signal peptide-contenting proteins HSPP-1 to HSPP-14. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, cardiovascular and antiasthmatic activities, and can be used to treat or prevent disorders associated with facreased activity or function of HSPP. Antagonists of HSPP associated with increased activity or function of HSPP. Such diseases include cell proliferation controlly; or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, corproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisenses, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antial therapeutic agents). As are used to diagnose, or monitor, HSPP related diseases (in usual immunosasys), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural
                                                                                                                                                                                                                                                               New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
                                                                                            Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                           AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 192-193; 327pp; English.
98US-0112129P
                                               (INCY-) INCYTE PHARM INC
                                                                                                                                                                                           WPI; 2000-160673/14.
                                                                                                                                                                                                                  N-PSDB; AAZ98155
11-DEC-1998;
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Sequence 383 AA;

ö Gaps ö 96.8%; Score 2044; DB 3; Length 383; 98.4%; Pred. No. 1.1e-141; Indels 2 1; Mismatches Matches 377; Conservative Query Match Best Local Similarity

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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG

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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 301 TYDLLYQQCDAQPGASGYGVYVRMWKRQQQXWERKIIGIFSGHQWVDMNGSPQDFNVAVR

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361 ITPLKYAQICYWIKGNYLDCREG 383

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361 ITPLKYAQICYWIKGNYLDCREG 383 음

AAY5362

AAY53627 standard; protein; 383 AA

AAY53627;

22-FEB-2000 (first entry)

A bone marrow secreted protein designated BMS192.

Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-euppression; megakarycoyte; platelet; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; parastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage amage; artificial joint.

Homo sapiens.

/note= "signal peptide' cocation/Qualifiers Peptide

WO9933979-A2

08-JUL-1999

98WO-US027008. 18-DEC-1998; 97US-0068958P. 98US-0101603P. 98US-0102540P. 24-SEP-1998; 30-DEC-1997;

CHIR) CHIRON CORP.

Lin H, Cao L;

WPI; 2000-038344/03. N-PSDB; AAZ36233. New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.

Claim 2; Page 81-82; 120pp; English.

AAY53622-43 represent bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiasis, and to treat myeloid or lymphoid cell incomparation of erythroid progenitor cells, and to treat various anamias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelosupport the growth and proliferation of myeloid cells such as granulocytes, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation with platelet transfusions, to treat stem cell disorders such as ablastic anamia and parcoxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions

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and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints
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                                                                                                                                                                                     1 MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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                                                                                                                   96.8%; Score 2044; DB 3; Length 383; 98.4%; Pred. No. 1.1e-141; ive 1; Mismatches 5; Indels (
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                                                                                                                                 Local Similarity 98.4
                                                                                     Sequence 383 AA;
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Greene JM;
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Best Local S:
Matches 377,
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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80666-A80623 encode the 12 secreted protein sequences given in AAA80665-A8063 encode the 12 secreted proteins sequences given in AAAB616-A80633. The human secreted proteins have various activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; cantiarthritic; antirheumatic, dermatological; antibacterial; antibacterial; antiarthritic; antiarthritic; antiarthritic; antichencer; vulnerary; antiviral; antibacterial; antiarthritic; and antifungal activity. The proteins, polypeptides, agonists and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermattis, and multiple collections examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermattitis, and multiple coronis disease, and nephritis; hyperproliferative disorders such as proteins and purpura; cardiovascular disorders e.g. coronary coronis and polymucleotide sequences may also be used in wound healing and protein sequences may also be used in wound healing and protein sequences may also be used in wound healing coronis and may also be used in sequences AAA85616-AB25618 represent alternative secreted protein gene #10 is located on chromosome 12.
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                                     for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
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                                                                                                                                                           Disclosure; Page 169; 803pp; English.
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                  WPI; 2000-387742/33
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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAB25576-B2559. The human secreted proteins sequences given in AAB25576-B2559. The human secreted proteins have various activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermaclogical; antiproliferative; antirheumatic, darmaclogical; antiproliferative; antiarthritic; antirheumatic; unless to proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic; antiarthritic; anticheumatic; dermaclogical; antiproliferative; antiagonise may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, theumatory disorders e.g. inflammatory disorders e.g. inflammatory disorders e.g. inflammatory disorders e.g. inflammatory disorders e.g. cronary paraproteinaemias and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
                                                                                                                                                                                                                multiple sclerosis; inflammatory disorder; inflammatory bowel disease; Crobn's disease; paphritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myccarditis; cancer; melanoma; lymphoma; wound healing; human; chromosome 12.
                                                                                                                                                    antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
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                                                                                                                             Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                                                   Protein encoded by human secreted protein gene #10 clone HUSQ05
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Pred. No. 1.1e-141;
1; Mismatches 5;
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il Similarity 98.4%;
377; Conservative
                                          (first entry)
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Best Local S:
Matches 377
  AAB25592,
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Wei

Moore PA,

Kenny JJ,

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The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynucleotides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollinger-
                                                                                        121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
                                                                                                                                                                            181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
                                                                                                                                                                                                               300
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                                                                                                                                                                                                                                                                                                     antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; antiarterioric; cardiant; antidathmatic; antiarthritic; antiarteriosclerotic; cardiant; antidatelic; cerebroprotective; thrombolytic; immunomodulator; enterocolitis; zollinger-Ellison syndrome; gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease; Alzaimer's ALS, neuropathy; dermal scarring; wound healing; nerve repair; thrombosis; bone; cartilage formation; angiogeneais; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
                    61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
61 VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS
                                                                     SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG
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WPI; 2001-081051/09
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                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ,
Filvaroff E,
08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
05-OCT-1999;
30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          Mather JP, P
Williams PM,
                                                                                                                                                                                                                                                           05-JAN-2000;
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                                                                                                                                                                                             16-DEC-1999;
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             Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scartings and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, anglogenesis, asthma, rheumatord arthritis, multiple sclerosis, inflammatory disorders, atherosclerosis, cardiac injury, infertility, premature aging; AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human PRO protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SGKSRRKRQIYGYDSRPSIPGKDPLLNYPPSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
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  Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
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Best Local Similarity 98.4
Matches 377; Conservative
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26-JUL-1999;
28-JUL-1999;
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The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's diseases, parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemlas such as coronary ischaemla, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), inflammatory pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
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ME, Goddard A
Kljavin IJ;
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                                                                                   99WO-US023089.
99WO-US028214.
99WO-US028864.
99WO-US028665.
99WO-US030095.
99WO-US030999.
99WO-US020944.
99WO-US021090.
99WO-US021547.
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61 VSSSCGPOCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS
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2000US-0189328P.
2000WO-US006884.
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21-MAR-2000;
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14-MAR-2000;
15-MAR-2000;
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29-MAR-2000;
29-MAR-2000;
30-MAR-2000;
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04-APR-2000;
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11-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human Zsigl3 proteins (AAB48972-B48974), and to DNA encoding them (AAC91782-C91784). The invention also relates to expression vectors and host cells comprising a human Zsigl3 DNA, and the recombinant production of a human Zsigl3 protein or its precursor. Zsigl3 is a serine protease, and has significant homology to Bacillus licheniformis glutamyl endopeptidase, human clotting factor X, human elastase, rat mast cell protease, Streptomyces griseus trypsin, bovine trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human Zsigl3 is located on chromosome 1122.1. Zsigl3 is useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing compositions. It may also be used in industrial applications in which proteases are utilised, including food processing, brewing and alcohol production, and as a component of a laundry detergent. The present sequence represents a human Zsigl3 variant
301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                                                                                                                                               Human Zsigl3; serine protease; chromosome 11q22.1; elastase homologue; glutamyl endopeptidase homologue; factor X homologue; trypsin homologue; trypsinogen homologue; mast cell protease homologue; collagenase homologue; protein degradation; food processing; brewing; alcohol production; laundry detergent component.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAGIPGLEFLLEFLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated serine protease (designated Zsig13), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications
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                                                                                                                                                                                                                                                Human Zsig13 variant #3, SEQ ID NO:18.
                                                  361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                 AAB48974 standard; protein; 383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Col 41-44; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0044185P.
98US-00062142.
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
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N-PSDB; AAC91784.
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Best Local S:
Matches 377,
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AAB48974
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180
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                                                                                                                                       300
                                                                                                                                                      241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                                                       TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell; proliferation; cell differentiation; colon; adrenal; hung; breast; prostate; rectum; cervix; liver; genetic disorder.
61 VSSSCGPQCHKGTPLPTYEBAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
                                     SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG
                                                                                       KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                                       IGMDYDYALLELKKPHKRKFMKIGVSPPAKOLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                          TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                                                                                                                                                                                                                                            ITPLKYAQICYWIKGNYLDCREG 383
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2000US-0198585P.
2000US-0199397P.
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18-APR-2000;
25-APR-2000;
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301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                                                                                                                                                                          Human, PRO, cytostatic, tumour, cancer; breast, lung, stomach, liver,
dog, cat; cow; horse, sheep, pig, goat, rabbit, ADEPT,
antibody-dependent enzyme mediated prodrug therapy.
                                                     361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                        361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                      ABUS8424 standard; protein; 383 AA.
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9705-0069425P
9705-006917P
9805-0077632P
9805-0077632P
9805-0077632P
9805-007886P
9805-007896P
9805-0079786P
9805-0079786P
9805-0080194P
9805-0080337P
9805-0080337P
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9805-0081195P
9805-0081195P
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97US-0062250P.
97US-0063486P.
97US-0063120P.
97US-0063121P.
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97US-0063541P.
97US-0063544P.
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97US-0063734P.
97US-0063870P.
97US-0064103P.
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97US-0066120P.
97US-0066466P.
97US-0066772P.
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98US-0083496P
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                                                                                                                                                                                                                                                                          Human PRO polypeptide #25.
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                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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24-0CT-1997;
24-0CT-1997;
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28-0CT-1997;
31-0CT-1997;
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21-NOV-1997;
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12-DEC-1997;
17-DEC-1997;
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20-MAR-1998;
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31-MAR-1998;
01-APR-1998;
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29-APR-1998;
29-APR-1998;
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10-MAR-1998;
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ABUS8424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of detect the presence of a tumour in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, catle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNP) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also proteins can be used to determine the presence of tumours and also breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
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Smith V, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                  2000WO-US023328.
2000WO-US030952.
2000WO-US032678.
2000WO-US034956.
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2000US-0209832P.
2000WO-US020710.
2000US-0199550P
2000US-0199654P
                               2000US-0201516P
                                                 2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
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                              03-MAY-2000;
17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
05-JUN-2000;
28-JUL-2000;
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24-AUG-2000;
08-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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PR 02-UUL-1998 9908-0091622P
PR 24-UL-1998 9908-0091622P
PR 24-UL-1998 9908-009528P
PR 10-AUG-1998 9908-009528P
PR 10-AUG-1998 9908-009528P
PR 11-AUG-1998 9908-009568P
PR 11-AUG-1998 9908-00958P
PR 11-AUG-1998 9908-00958P
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PR 11-AUG-1998 9908-009592P
PR 11-AUG-1998 9908-009992P
PR 11-AUG-1998 9908-001039P
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MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE

Search completed: July 1, 2005, 21:03:26 Job time : 104.435 secs THIS PAGE BLANK WSPTON

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NAME/KEY: Signal Sequence LOCATION: 1...19
COTHER INFORMATION:
US-09-072-384-2
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ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 392 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein FRAGMENT TYPE: internal
single
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STRANDEDNESS: sing
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US-09-072-384-2
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 10, Appl
1, Appli
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3471, Ap
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2, Appli
                                                              July 1, 2005, 20:57:14; Search time 26.5364 Seconds (without alignments) 1102.727 Million cell updates/sec
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                                                                                                                          1 MAGIPGLLFLLFFLLCAVGQ......IKGNYLDCREGDTVFLPGSN 392
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Sequence 261
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('Ggn2_6')ptodata'1/iaa'5B_COMB.pep:*

('Ggn2_6')ptodata'1/iaa'6A_COMB.pep:*

('Ggn2_6')ptodata'1/iaa'6B_COMB.pep:*

('Ggn2_6')ptodata'1/iaa'PCTUS_COMB.pep:*

('Ggn2_6')ptodata'1/iaa'APCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-551-826D-14
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-09-107-433-3471
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US-08-639-075A-89
US-09-012-431-89
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                                                                                                                                                                         513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2112
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Match Length
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28 123 5.8 256 3 US 09-012-692-89 Sequence 89, Appl 121 123 5.8 256 3 US 09-012-692-89 Sequence 89, Appl 122 5.8 256 3 US 09-012-692-89 Sequence 89, Appl 122 5.8 256 3 US 09-012-692-1442A-89 Sequence 19, Appl 123 121.5 5.8 226 4 US-09-645-95A-1389 Sequence 12, Appl 24 121.5 5.8 226 4 US-09-645-95A-1389 Sequence 12, Appl 24 121.5 5.8 226 4 US-09-645-95A-1389 Sequence 12, Appl 24 121.5 5.8 226 4 US-09-645-95A-1389 Sequence 12, Appl 25 121.5 5.8 427 1 US-09-647-037-2 Sequence 12, Appl 26 121.5 5.8 427 1 US-09-647-037-2 Sequence 12, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-09-647-037-2 Sequence 27, Appl 27 121.5 5.8 427 1 US-
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                                                                                                                                                        61 VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
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                                                                               1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                        Gaps
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
TITLE OF SEQUENCES: 18
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
Query Match 99.6%; Score 2104; DB 3; Length 392; Best Local Similarity 100.0%; Pred. No. 5.2e-218; Matches 392; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 ITPLKYAQICYWIKGNYLDCREGDTVFLPGSN 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ITPLKYAQICYWIKGNYLDCREGDTVFLPGSN 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLESSEE: ZYMOGENETICS, INC.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98107
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Patent No. 6153420
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER:
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US-09-072-384-15
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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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US-09-072-384-18
i Sequence 18, Application US/09072384
j Patent No. 6153420
j GENERAL INFORMATION:
    APPLICANT: Sheppard, Paul O.
    ITILE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM NUMBER OF SEQUENCES: 18
    CORRESPONDENCE ADDRESS: ADDRESSE: ZymoGenetics, Inc.
    STREET: 1201 Eastlake Avenue East
    CITY: Seattle
    STATE: WA
    COUNTRY: USA
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                   Length 392;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                 98.7%; Score 2085; DB 3;
98.2%; Pred. No. 5.9e-216;
rative 1; Mismatches 6;
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MEDIOT TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
                                                                                                         NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.23
Matches 385; Conservative
                 TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
PEATURE:
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single
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STRANDEDNESS:
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181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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Pred. No. 1.5e-211;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT PILING DATE: 2001-07-17

PRIOR PILING DATE: 2000-02-2

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-07

PRIOR PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12
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Wood, William, I.
                                                                                                                 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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98.4%;
                                         ljavin, Ivar J.
lather, Jennie P.
an, James
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Best Local Similarity 98.4
Matches 377; Conservative
                                                                                                                                                                                                                 Jumas, Daniel
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US-09-907-794A-261
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Pred. No. 1.5e-211;
1; Mismatches 5;
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                                REFERENCE/DOCKET NUMBER: 97-16C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 261, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
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Grimaldi, Christopher J.
REGISTRATION NUMBER: 31,648
                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 383 anino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Signal Sequence LOCATION: 1...19
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Best Local Similarity 98.4%;
Matches 377; Conservative
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Gerritsen, Mary B
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                                                                                                                 TELEFAX: 206-442-6678
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION:
US-09-072-384-18
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96.8%; Score 2044; DB 4;
98.4%; Pred. No. 1.5e-211;
iive 1; Mismatches 5;
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30091
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PLILOR DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILOR DATE: 1999-12-30
PRIOR PLILOR DATE: 1999-12-30
PRIOR PLILOR DATE: 2000-01-05
SEQ ID NOS: 423
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Patent No. 6686411
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wai-Qiang
Gerber, Hanspeter
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Best Local Similarity 98.4
Matches 377; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo Sapien
US-09-905-125A-261
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APPLICANT:
APPLICANT:
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  241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                                     301 TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                    241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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Patent No. 6664376
GENERAL INPORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eston, Dan L.
APPLICANT: Eston, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Hillan, Kenneth,
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Mather, Jennie P.
Pan, James
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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300 241 IGMDYDYALLELKKPHKRKFWKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG 1 MAGIPGLEFLEFELCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE 61 VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR Gaps ; 0 Length 383, Indels

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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                     301 TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                           301 TYDLLYQQCDAQPGASGSGVYVRWWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
  181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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APPLICATION NUMBER: PCT/US99/20594
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PPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/23089
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: US 60/145,698
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APPLICATION NUMBER: US 60/146,222
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Patent No. 6723535
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Hilvaroff, Ellen
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ather, Jennie P.
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Ashkenazi, Avi
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Eaton, Dan L.
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Pred. No. 1.5e-211;
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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FILING DATE: 1999-12-02
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FILING DATE: 1999-12-16
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FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 383
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APPLICATION NUMBER: PCT/US99/20944
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PRIOR APPLICATION NUMBER: US 60/143,048
RRIOR FILING DATE: 1999-07-07
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FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
                                                                                                                                                       Williams, P. Mickey Wood, William, I.
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tewart, Timothy A.
umas, Daniel
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98.4%;
                                                                Nicholas F.
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Kljavin, Ivar J.
Mather, Jennie P.
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Best Local Similarity 98.4
Matches 377; Conservative
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US-09-902-775A-261
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98.4%; Pred. No. 1.5e-211;
iive 1; Mismatches 5;
                                               APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12.
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-07-11
PRIOR PPLICATION NUMBER: PCT/US00/04114
PRIOR APPLICATION NUMBER: BC1/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
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PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-12-02
  Jennie P.
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Best Local Similarity 98.4<sup>†</sup>
Matches 377; Conservative
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; ORGANISM: Homo Sapien
US-09-903-603A-261
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Pred. No. 1.5e-211;
1; Mismatches 5;
                   PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
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Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Becstein, David
APPLICANT: Becstein, David
APPLICANT: Becsoyers, Luc.
APPLICANT: Becon, Dan L.
APPLICANT: Extrara, Napoleone
APPLICANT: Ferrara, Napoleone
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Best Local Similarity 98.4%;
Matches 377; Conservative
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Gerritsen, Mary E.
Goddard, A.
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Gao, Wei-Qiang
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CORGANISM: Homo Sapien
US-09-906-700-261
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US-09-903-603A-261
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61 VSSSCGPQCHKGTPLPTYBEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240 61 VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG 180 9 1 MAGIPGLIFELLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE Gaps .. 0 Length 383,

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61 VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
PRIOR APPLICATION NUMBER: PCI/USSS/20005
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-05
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USS9/30999
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
PRIOR PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerritsen, Mary E
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Hillan, Kenneth,
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Best Local Similarity 98.43
Matches 377; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Mather, Jennie
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Eaton, Dan L.
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                 , TYPE: PRT
, ORGANISM: Homo Sapien
US-09-904-920A-261
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US-09-909-064-261
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wool, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT APPLICATION NUMBER: US/00/0414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR APPLICATION NUMBER: PCT/US99/21647
                                                          301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                       301 TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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PRIOR FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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5.09-904-920A-261
5.Sequence 261, Application US/09904920A
7.Patent No. 6806352
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Grimaldi, Christopher J
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ilvaroff, Ellen
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Kljavin, Ivar J.
Mather, Jennie P.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Eaton, Dan L.
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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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Godowski, Paul J.
Gofowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBENCE: 1046-6-1.
FILE REPERBENCE: 1046-1.
FILE REPERBENCE: 1046-1.
FRIOR APPLICATION NUMBER: US/09/909,064
CURRENT APPLICATION NUMBER: D60/1-07-180
PRIOR FILING DATE: 1999-07-2.
FRIOR FILING DATE: 1999-07-2.
FRIOR FILING DATE: 1999-07-2.
FRIOR PELLING DATE: 1999-07-2.
FRIOR PELLING DATE: 1999-07-2.
FRIOR PELLING DATE: 1999-07-2.
FRIOR PELLING DATE: 1999-09-15
FRIOR PELLING DATE: 1999-10-05
FRIOR PELLING DATE: 1999-11-20
FRIOR P
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Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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ORGANISM: Homo Sapien
US-09-909-064-261
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241 IGMDYDYALLELKKPHKRKFWKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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                                                                                                               APPLICANT: Willians, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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Pred. No. 1.5e-211;
1; Mismatches 5;
                                                                                                                                                                                                                                    FILE REFERENCE: 1046-14

CURRENT PAPLICATION NUMBER: US/09/906,618

CURRENT FILING DATE: 2001-07-16

PRIOR PAPLICATION NUMBER: US/0143,048

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/2095

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-16

PRIOR PILING DATE: 1999-12-26

PRIOR PILING DATE: 1999-12-16

PRIOR PILING DATE: 1999-12-26

PRIOR PILING DATE: 1999-12-36

PRIOR PILING DATE: 1999-12-36
                                                                     Timothy A.
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Best Local Similarity 98.4
Matches 377; Conservative
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                                                                     ewart,
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Pred. No. 1.5e-211;
1; Mismatches 5;
361 ITPLKYAQICYWIKGNYLDCREG 383
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Patent No. 6828146
GENERAL INFORMATION:
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.4%;
Matches 377; Conservative
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ilvaroff, Ellen
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Gerritsen, Mary E.
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Saton, Dan L.
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US-09-905-381A-261
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                                                                                                                                        SEQ ID NO 2
LENGTH: 316
TYPE: PRT
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 TPL---PTYKBAKQYLSYETLYANGSRTEXQVGIYILSSSGDG-----AXXRDSGSSG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 TPVSSDPSYKPGSTYDPNIKIDNNGA-----YSKAFEGTGTPGGSVQAKPKKESPAG 86
241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                   301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
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APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Christensen, Claus Bo Voge
APPLICANT: Lassen, Soren Flensted
TITLE OF INVENTION: No. 6558939el Ptoteases And Variants Thereof
FILE REFERENCE: 5665.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Bacillus licheniformis AC116
                                                                                                                                                                                                                                                                                                    361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                                       361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09551826D Patent No. 6558939
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Patent No. 6558939
GENERAL INFORMATION:
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US-09-551-826D-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 PAGPRYSPKSVIGSDERTRVTN---TTAYPYRAIVHISSSIGSCTGSLIGPKTVATAGHC 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 SSGKSRRK------RQIYGYDSRFSIFGKDFLLNYPFSTSVKLST---GCTGTLVAE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 THVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 YFIPSGWRSGNTN-----YDYGAIELSEPIGNTVGYFGYSYTTSSLVGTTVTISGYPGDK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 PGNLVYRFCD--VKDETYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKII----GIF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 TPVSSDPSYKPDSS-ASYDPAIKTNKN----GAYSKAFEGTGKLDAPLYQEKSKPTKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 XHVLTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKR
                                                                                                                                                                                                                                                                                                                                                        Gaps
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APPLICANT: No. 6558939regaard-Madsen, Mads
APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Christenesn, Claus Bo Voge
APPLICANT: Lassen, Soren Flensted
TITLE OF INVENTION: No. 6588939el Ptoteases And Variants Thereof
FILE REFERENCE: 5665.200-US
CURRENT APPLICATION NUMBER: US/09/551,826D
                                                                                                                                                                                                                                                                                              Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 318
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Best Local Similarity 23.1%; Pred. No. 4e-09;
Matches 76; Conservative 32; Mismatches 143; Indelb
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                                                                                                                                                                                                                                                                                        Query Match

8.7%; Score 184; DB 4; L
Best Local Similarity 23.2%; Pred. No. 4.5e-11;
Matches 77; Conservative 46; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 SGHOWVDMNGSPODFNVAVRITPLKYAQICYW 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SSYNRGTRITKEVFDNLTNW 311
CURRENT APPLICATION NUMBER: US/09/551,826D CURRENT FILING DATE: 2000-04-17 WUMBER OF SEQ ID NOS: 14 SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus licheniformis CDJ31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09551826D Patent No. 6558939
                                                                                                                                                                                                , ORGANISM: Bacillus licheniformis US-09-551-826D-2
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Search completed: July 1, 2005, 21:10:42 Job time: 29.5364 secs

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US-09-765-205-12
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2112
1 MAGIPGLLFLLFFLLCAVGQ.....IKGNYLDCREGDTVFLPGSN 392
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19: /cgn2_6/ptodata/1/pubpaa/USIOB_RUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                       OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 12, Appl	261,	261,	261,	261,	261,	261,	261	Sequence 261, App	Sequence 261, App	Sequence 261, App
SUMMARIES	. QI	US-09-765-205-12	US-09-909-320-261	US-09-909-088B-261	US-09-905-291A-261	US-09-902-853-261	US-09-907-824-261	US-09-907-841-261	US-09-904-011-261	US-09-903-640-261	US-09-908-093-261	US-09-906-742-261
	DB	6	6	0	σ	6	σ	σ	10	70	20	10
	Query Match Length DB	383	383	383	383	383	383	383	. 383	383	383	383
*	Query Match	96.8	96.8	96.8	96.8	96.8	96.8	96.8	96.8	96.8	96.8	96.8
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
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8.96	96.8	96.8	8.96	96.8	96.8	96.8	96.8	96.8	96.8	96.8	96.8	8.96	96.8	96.8	8.96	8.96	96.8	8.96	96.8	96.8	96.8	96.8	96.8	96.8	96.8	96.8	96.8	8.96	96.8	96.8	8.96	8.96	8.96
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ALIGNMENTS

SGKSRRKRQIYGYDSRPSIFGKOPLLNYPPSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG 180 9 9 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE Gaps Sequence 12, Application US/09765205
Patent No. US20020034800A1
GENERAL INFORMATION:
APPLICANT: Cao, Li
TITLE OF INVENTION:
APPLICANT SPALICATION UNBER: US/09/765, 205
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/09/212,440
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12 ö Query Match 96.8%; Score 2044; DB 9; Length 383; Best Local Similarity 98.4%; Pred. No. 4e-193; Matches 377; Conservative 1; Mismatches 5; Indels ORGANISM: human US-09-765-205-12 121 TYPE: PRT g ò g ò ò

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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapien
US-09-909-320-261
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MOCOL, MILLIAM, 1.
MILLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE SERERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR PLING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-38
PRIOR FILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-10-05
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121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
                                                                                                                         241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
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Patent No. USZ0020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bostsein, David
APPLICANT: Bestsein, David
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Macher, Jennie P.
Pani, James
Pani, Nicholas F.
Roy, Margaret Ann
Stewart, Timchy A.
Tumas, Daniams, P. Mickey
Wood, Williams, I.
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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96.8%; Score 2044; DB 9; Length 3
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-00
PRIOR FILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US09/3099
PRIOR FILING DATE: 2000-01-05
NUMBER: PCT/US09/3099
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
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Patent No. US20020146709A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filonoff, Ellen
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Gao, Wei-Qiang
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AFFLICANT:
MOOG, WILLIAM, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT PAPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PELICATION NUMBER: PCT/US99/2094
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
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                                                       301 TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                              181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
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Patent No. US20020160374A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Williams, P. Mickey
Wood, William, I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Mather, Jennie P.
Pan, James
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/909,088B

CURRENT FILING DATE: 2001-07-18
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PRIOR PLLING DATE: 1999-105
PRIOR PLLING DATE: 1999-10-15
PRIOR PLLING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PLLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLLING DATE: 1999-12-02
PRIOR PLLING DATE: 1999-12-02
PRIOR PELLING DATE: 1999-12-16
PRIOR PELLING DATE: 1999-12-16
PRIOR PELLING DATE: 1999-12-16
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILLING DATE: 1999-12-20
PRIOR PELLING DATE: 1999-12-20
PRIOR PELLING DATE: 2000-01-05
PRIOR PELLING DATE: 2000-01-05
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PRIOR PELICATION NUMBER: PCT/US00/04414
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/21547
Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                         Gurney, Austin L.
Hillan, Kenneth, J
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                                                                             Kljavin, Ivar J.
Mather, Jennie P.
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CRGANISM: Homo Sapien
US-09-909-088B-261
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LENGTH: 383
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              PRIOR FILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-10
PRIOR PLING DATE: 1999-12-00
PRIOR PLING DATE: 1999-12-00
PRIOR PLING DATE: 1999-12-00
PRIOR PELING DATE: 1999-12-00
PRIOR PELING DATE: 1999-12-00
PRIOR PELING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
APPLICATION NUMBER: PCT/US99/28313
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US-09-902-853-261
; Sequence 261, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.;
; APPLICANT: Botherin, David
; APPLICANT: Botherin, David
; APPLICANT: Besnoyers, Luc
; APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, A.
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APPLICANT:
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APPLICANT:
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### PRPLICANT: WILLIAMS, P. MIZCKAY
# APPLICANT: WILLIAMS, P. MIZCKAY
# APPLICANT: WILLIAMS, P. MIZCKAY
# APPLICANT: WILLIAMS, P. MIZCKAY
# TITLE OF INVERTION: Secreted and Transmembrane Polypeptides and Nucleic
# CTREENER TO LINGE-14

CURRENT APPLICATION NUMBER: US/09/902,853

CURRENT PLING DATE: 2000-07-10

PRIOR FILING DATE: 1999-00-18

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-16

PRIOR PLING DATE: 1999-09-16

PRIOR PLING DATE: 1999-09-16

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-05

PRIOR PRIOR PLING DATE: 1999-12-05

PRIOR PRIOR DATE: 1999-12-05

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PRIOR PRIING DATE: 2000-01-05

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                                                                                                                                                                                                                                                                        Williams, P. Mickey Wood, William, I.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                        Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                             Timothy A.
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Best Local Similarity 98.4
Matches 377; Conservative
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US-09-902-853-261
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121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-30
PRIOR PELLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PLING DATE: 2000-01-05
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Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc.
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone;
APPLICANT: Filvaroff, Ellen
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Goddard, A.
Godowski, Paul J.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Best Local Similarity 98.4
Matches 377; Conservative
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US-09-907-824-261
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LENGTH: 383
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                                  101 TYDLLYQQCDAQPGASGSGVYVRWWKRQQQKWERKIIGIFSGHQWVDMNGSPQDENVAVR 360
         KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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PRIOR APPLICATION NUMBER: 09/665,350
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28214
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5. US20020197671A1
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Publication No. US20
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-20

FRIOR PELICATION NUMBER: PCT/US00/04414

PRIOR PELICATION NUMBER: PCT/US00/04414

PRIOR PELICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PELING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-29
                                                                                                                                                                                                APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: William B. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 4e-193;
1; Mismatches 5; Indels
Grimaldi, Christopher J. Gurney, Austin L. Hilan, Kenneth, J. Kljavin. Ivar J. Mather, James Pan, James Paoni, Nicholas F.
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Best Local Similarity 98.4%;
Matches 377; Conservative
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ORGANISM: Homo Sapien
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APPLICANT: WOOd, Willilam, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: 1046-14

CURRENT APPLICATION NUMBER: US/09/904.011

CURRENT APPLICATION NUMBER: US/09/65.350

PRIOR PELING DATE: 2001-07-15

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-36

PRIOR PLING DATE: 1999-07-36

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-
Sequence 261, Application US/09904011
Publication No. US20030003530A1
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Pred. No. 4e-193;
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                       Acids Encoding the Same
                  TITLE OF INVENTION: Acids Encoding the Se
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,640
PURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
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Publication No. US20030017498A1
GENERAL INPORMATION:
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Grimaldi, Christopher J.
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Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Hillan, Kenneth, J
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Roy, Margaret Ann
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity 98.4<sup>3</sup>
Matches 377; Conservative
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; ORGANISM: Homo Sapien
US-09-903-640-261
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LENGTH: 383
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                                                                                                                                                                             96.8%; Score 2044; DB 10; Length 383;
98.4%; Pred. No. 4e-193;
Live 1; Mismatches 5; Indels 0
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
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Grimaldi, Christopher J.
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Wood, William, I.
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Filvaroff, Ellen
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Kljavin, Ivar J.
Mather, Jennie P.
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botselin, David
APPLICANT: Beton, Dan L.
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Best Local Similarity 98.4
Matches 377; Conservative
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                                                                                                        TYPE: PRT

ORGANISM: Homo Sapien

US-09-904-011-261
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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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Publication No. US20030023054A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, David
APPLICANT: Baton, David
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Gerritsen, Mary E
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Mather, Jennie P.
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** APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, P. Milliam, P. Milliam, P. Milliam, P. Milliam, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TILE OF INVENTION: Acids Encoding the Same CURRENT FILING DATE: 10466-14

CURRENT APPLICATION NUMBER: US/09/908,093

CURRENT FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: D6/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-36

PRIOR PLING DATE: 1999-07-36

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-18

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15
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Pred. No. 4e-193;
1; Mismatches 5;
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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Best Local Similarity 98.4%;
Matches 377; Conservative
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US-09-908-093-261
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APPLICANT: Tunas, Danie,
APPLICANT: Tunas, Danie,
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, D.
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10466-14
CURRENT PEPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-18
FRIOR PELING DATE: 2000-05-18
FRIOR PELING DATE: 2000-05-22
FRIOR APPLICATION NUMBER: OF (6143,048
FRIOR PELING DATE: 1999-07-07
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-08
FRIOR PELING DATE: 1999-09-15
FRIOR PELING DATE: 1999-10-15
FRIOR PELING DATE: 1999-10-15
FRIOR PELING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-20
                                           TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
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KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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                                                                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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Pred. No. 4e-193;
.; Mismatches 5;
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/906,838 CURRENT FILING DATE: 2001-07-16
                                                                                   Williams, P. Mickey Wood, William, I.
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98.4%;
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Best Local Similarity 98.4
Matches 377; Conservative
                                                                   Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-261
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Pred. No. 4e-193;
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        PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
APPLICATION NUMBER: PCT/US99/28565
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Publication No. US20030027143A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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98.4%;
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Filvaroff, Ellen
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Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Best Local Similarity 98.4
Matches 377; Conservative
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APPLICANT:
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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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Pred. No. 4e-193;
1; Mismatches 5; Indels 0
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30091
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Publication No. US20030027146A1
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, A.
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Best Local Similarity 98.4<sup>1</sup>
Matches 377; Conservative
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                     LENGTH: 383
TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT: Hillan, Kennech, J.
APPLICANT: Hillan, Ivar J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
FILE REFERENCE: 10466-14
FRIOR REPLICATION NUMBER: US 60/143,048
FRIOR PELICATION NUMBER: US 60/145,698
FRIOR PELICATION NUMBER: US 60/145,698
FRIOR PELICATION NUMBER: PCT/US99/20594
FRIOR PELICATION NUMBER: PCT/US99/20594
FRIOR PELICATION NUMBER: PCT/US99/21090
                                                      241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                            301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                     301 TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
         181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
                                                                                                      241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
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Publication No. US20030027145A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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APPLICANT: Ashkenzi, Avi
APPLICANT: Betetin, David
APPLICANT: Beton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/904,859

CURRENT APPLICATION NUMBER: US/065,350

REIOR PILING DATE: 2001-07-12

PRIOR PAPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-09-18

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

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PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

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Publication No. US20030036060A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenzi, Avi
APPLICANT: Bettein, David
APPLICANT: Beton, Dan L.
APPLICANT: Baton, Dan L.
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96.8%; Score 2044; DB 10; Length 383;
Best Local Similarity 98.4%; Pred. No. 4e-193;
Matches 377; Conservative 1; Mismatches 5; Indels 0
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PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-05
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USO0/04114
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/28214
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RICH REPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
                                                                                                                                    Williams, P. Mickey Wood, William, I.
                                                                                        Timothy A.
                                            Nicholas F.
                                                                loy, Margaret Ann
Stewart, Timothy ,
Tumas, Daniel
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Mather, Jennie P.
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Pred. No. 4e-193;
1; Mismatches 5; Indels 0
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR PILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-05
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Job time : 93.3582 secs
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Best Local Similarity 98.4%;
Matches 377; Conservative
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-859-261
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5.1.6 Compugen Ltd.	
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	using sw model
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	OM protein

Run on:

July 1, 2005, 20:54:23; Search time 20.826 Seconds (without alignments) 1811.048 Million cell updates/sec

US-09-658-677-2 2112 1 MAGIPGLLFILCAVGQ.....IKGNYLDCREGDTVFLPGSN 392 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	endopeptidase (EC	metalloproteinase	coagulation factor	choline binding pr	pancreatic elastas	pancreatic elastas	probable pancreati	coagulation factor	coagulation factor	pancreatic elastas	pancreatic elastas	trypsin (EC 3.4.21		pancreatic elastas	hypothetical prote		e E	complement factor	pancreatic elastas	brain-specific ser	choline binding pr	probable secreted	T-cell suppressor	pancreatic elastas	hypothetical prote		hypothetical prote	hypothetical prote	serine proteinease
SUMMARIES																														
SUMM	ID	A45134	A35122	EXRT	E97915	B26823	S70439	A56615	EXHU	EXBO	A26823	A25528	TRSMG	ELPG	ELRT1	T29767	TRWVSY	A59271	DBHU	C26823	JC5759	C95045	T35117	A28566	ELRT2	E85765	H64915	T15308	T31617	A47547
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عد	Query	8.8	6.2	5.9	5.9	5.6	5.4	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.3	2.5	5.2	5.1	5.1	5.0	5.0	4.9	4.9	4.9	9.	4.8
	Score	185	130.5	125	124	118	114	114	114	114	113	113	112.5	112	112	112	111.5	111.5	111	110	109	107.5	107.5	106	106	104.5	104.5	104.5	102.5	102
	Result No.	-	7	e	4	2	9	7	ω	Ð	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

probable pepetidas complement factor	complement factor masquerade precurs	trypsin-related pr allergen Der f III	trypsin-like prote coaqulation factor	probable secreted coagulation factor	hypothetical prote adenylate cyclase	trypsin-like prote	membrane-bound arg	coagulation factor
AH0282 A29154	I51579 A55617	S40004 S68424	JC4170 KFBO7	T35118 KFBO	T34929 JC4747	JC4850	JC7731	A30351
0 0	0 0	0 0	7	24	~ ~	~ ~	4 (4	-
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27.	1047	274	272	409	1238	266	855	452
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	4.4 8.8	4.4	4. 4. 6. 0.		2.5		. 4. ∪ ∩	93.5 4.4 452

ALIGNMENTS

70; 46; Mismatches 139; Indels 77; Conservative Matches : | : | : | : | | : : | | : : | | : : | | : : | 177 TKEKAEKKSPAKAPYSIKSVIGSDDRTRVTN---TTAYPYRAIVHISSSIGSCTGWMIGP 133 120 SSGKSRRK------ROIYGYDSRFSIFGKDFLLNYPFSTSVKLST---GCTGTLVAE 167 168 XHVLTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKR 226 227 THVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDR 286 287 PGNLVYRFCD--VKDETYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKII----GIF 340 ò g ò В δ 셤 ò g ò

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Oy 341 SCHQWVDMNGSPQDFNVAVRITPLKYAQICYW 372 Db 290 GGSSYNRGFRITKEVFDNLFNW 311	Db 158 TITAAPGRNGSSYPYGTYSGTMFYSVK-GWTESKDTNYD 195 Qy 231 KGWIKGNANDIGMDYDYALLELKKPHKRKFWKIGVŞPPAKQLPGGRIHPSGYDNDRP, 287
RESULT 2 A35122 metalloproteinase (EC 3.4) mpr precursor, extracellular - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 27-Jul-1990 #sequence revision 27-Jul-1990 #text_change 16-Aug-2004 C;Accession: A35122; I40010; Ā6966 R;SJOma, A.; Rudolph, C.F.; Rufo Jr., G.A.; Sullivan, B.J.; Theriault, K.A.; Ally, D.; F J. Bacteriol. 172, 1024-1029, 1990 A;Title: Gene encoding a novel extracellular metalloprotease in Bacillus subtilis. A;Reference number: A35122; MUID:90130256; PMID:2105291	Db 196 YGAIKLNGSPGNTVGW-YGYRTTNSSSPVGLSSSVTGFPCDKTFGTMWSDTKP 247 Qy 288 GNLVYRFCDVKDETYDLLYQQCDAQPGASGYGVVRMWKRQQQKWERKIIGIFSGHQWVD 347 Db 248 IRSAETYKLTY-TTDTYGCQSGSPVYRNYSDTGQTAIAIHT 287 Qy 348 MNGSPQDFNVAVRITPLKYAQICYW 372 Db 288 -NGG-SSYNLGTRVTNDVFNNIQYW 310
A;Accession: A53122 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-313 <55LO- A;Cross-references: UNIPROT:P39790; GB:L10505; NID:g143209; PIDN:AAA22604.1; PID:g143210 A;Cross-references: UNIPROT:P39790; GB:L10505; NID:g143209; PIDN:AAA22604.1; PID:g143210 R;Smith, H.; de Jong, A.; Bron, S.; Venema, G. Gene 70, 351-361, 1988 A;Title: Characterization of signal-sequence-coding regions selected from the Bacillus E A;Reference number: 139994; MUID:89108019; PMID:3145906 A;Accession: I40010 A;Accession: I40010 A;Molecule preliminary; translated from GB/EMBL/DDBJ	RESULT 3 EXRT Coagulation factor Xa (EC 3.4.21.6) precursor - rat C,Species: Attus norvegicus (Norway rat) C,Species: Attus norvegicus (Norway rat) C,Date: 31Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004 C,Accession: S49075; JC4670; FS0191; PS0190; I62745 R,Stanton, C.; Ross, P.; Hutson, S.; Wallin, R. Thromb. Res. 80, 63.73, 1995 A,Title: Evidence for competition between vitamin K-dependent clotting factors for intrace A,Reference number: A58498; MUID:96093366; PMID:8578539
A; Residues: 1-60,65,'L',67,'S',69,'AQA' <res> A; Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702 A; Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702 B; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bronn, S.; Bruustilet, S.; Bruuschi, C.V.; Caldwell, B.; Capuano, V.; Catter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Nature 390, 249-256, 1997 A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Lardinois, Levinors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, H.; Masulda, S.; Maueel A; Cawa, K.; Coriwara, A.; Cudega, R.; Park, S. H.; Park, S. H</res>	A; Molecule type: mRNA A; Residues: 1-482 <sta1> A; Residues: 1-482 <sta1> A; Residues: 1-482 <sta1> A; Coss-references: UNIPROT:Q63207; EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g5066(A; Note: neither the complete nucleic acid sequence nor the complete translation are shown R; Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R. Gene 169, 269-273, 1996 A; Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs. A; Reference number: JC4670; MUID:96194815; PMID:8647460 A; Molecule type: mRNA</sta1></sta1></sta1>
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toganoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wippt, A.; Yamamoto, H.; Yamame, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, K.; Yoshida, K.; Attle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377 A; Reference number: A69580; Mulb:sequence not shown; translation not shown A; Residues: 1-313 «KUN»	A;Residues: 1-462 <5TA2> A;Residues: 1-462 <5TA2> A;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601 A;Experimental source: Cos-1 cell R;Enjyoji, K.; Miyazaki, K.; Kato, H. J. Biochem. 109, 890-898, 1991 A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plast A;Reference number: PS0190; MUID:92041742; PMID:1718949 A;Reference number: protein A;Rocession: PS0191 A;Molecule type: protein A;Recession: PS0190
A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12018.1; PID:e1182176; A;Experimental source: strain 168 C;Genetics: A;Gene: mpr C;Superfamily: Glutamyl endopeptidase, V8 type C;Keywords: hydrolase Query Match Best Local Similarity 22.6%; Pred. No. 0.0018;	A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Residues: 183-186, 'X', 188-207 < ENJ2> R; Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y. Rur. J. Haematol. 52, 162-168, 1994 A; Title: Analysis of the partial nucleotide sequences and deduced primary structures of the A; Reference number: 146196; MUID:94222160; PMID:8168596 A; Reference number: I62745 A; Status: pretiminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
Vative 38; Mismatches 139; Indels 121; Gaps 19; LPVVLPQSTLNLARPDFGAEAKLEVSSSCGPQCHKGTPLPTYKEAK 82 :	A;Residues: 295-383, 'G', 385-455 <mur> A;Coss-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396 C;Function: C;Function: A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre A;Pathway: blood coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Keywords: beta-hydroxyaspartic acid, blood coagulation; calcium binding; carboxyglutami F;1-23/Domain: signal sequence #status predicted <sig> F;24-40/Domain: propeptide #status predicted <gro> F;24-40/Domain: Gadomain homology <gla> F;41-179/Product: coagulation factor X light chain #status predicted <lch> F;90-121/Domain: EGF homology <eg1> F;183-164/Domain: EGF homology <eg2> F;183-482/Product: coagulation factor X heavy chain #status predicted <hch> F;183-482/Product: coagulation factor X heavy chain #status predicted <hch> F;183-482/Product: coagulation factor X heavy chain #status predicted <hch> F;183-31/Domain: activation peptide #status predicted <apt></apt></hch></hch></hch></eg2></eg1></lch></gla></gro></sig></mur>

are

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A;Molecule type: mRNA
A;Residues: 1-269 <FLES
A;Cross-references: GB:M16631; NID:g182022; PIDN:AAA52374.1; PID:g182023
A;Cross-references: GB:M16631; NID:g182022; PIDN:AAA52374.1; PID:g182023
A;Shirasu, Y.; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, T.; J. Biochem. 102, 1555-1563, 1987
J. Biochem. 102, 1555-1563, 1987
A;Title: Molecular cloning and expression in Escherichia coli of a cDNA encoding human pt A;Reference number: A41431; MUID:88198076; PMID:2834346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P08217; GB:M16652; NID:g182057; PIDN:AAA52380.1; PID:g182058 R;Fletcher, T.S.; Shen, W.F.; Largman, C. Bicchenitzty 26, 7256-7261, 1987 A;Afitle: Primary structure of human pancreatic elastase 2 determined by sequence analysis A;Reference number: A27432; MUID:88107669; PMID:3427074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complexes involving procarboxyper
                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs A,Reference number: A90958; MUID:87217962; PMID:3646943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 DGGRG----ANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 HKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 SGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYA---QICYW 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GRHNLYVAESGSLA-----VSVSKIVVHKDW---NSNQISKGNDIALLKLANPV 131
                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: B26823; A27432; A41431; S34491
S;Kawashima, I; Tani, T.; Shimoda, K.; Takiguchi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 SWPWQVSLQYSSNGKWYHTCGGSLIANSWVLTAAHCISSSRTY-----RVGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-201,'V',203-269 <SHI>
A,Residues: 1-201,'V',203-269 <SHI>
A,Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1; PID:g219620
A,Note: the authors translated the codon GTG for residue 202 as Cys
R,Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C.
FEBS Lett. 261, 179-183, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Map position: Izpter-Izger
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-28/Domain: propeptide #status predicted <PRO>
F;29-269/Product: pancreatic clastase IIA #status predicted <P:29-262/Domain: trypsin homology <PRY>
F;29-262/Domain: trypsin homology <PRY>
F;73,121,216/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                          pancreatic elastase II (EC 3.4.21.71) A precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Further studies on the human pancreatic binary A,Reference number: S08253; MUID:90169111; PMID:2307232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---- TPNN ----
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A;Residues: 'X',18-50 <MOU>
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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-269 < KAW>
   358 AVRI 361
                                                                     202 AVKL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B26823
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                    F;232-460/Domain: trypsin homology <TRY>
F;46.47,54.56,96.06,66.69,72.79/Modified site: gamma-carboxyglutamic acid (Glu) #stat F;46.47,54.56,96.06,66.69,72.79/Modified site: gamma-carboxyglutamic acid (Glu) #stat F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;108/Binding site: carbohydrate (Asn) (covalent) #status predicted F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted F;218/Binding site: Arg-ile (coagulation factor IXa, coagulation factor VIIa) #stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cjaccession: E97915
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; P. R.; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Streptococcuâ pneumoniae (strain R6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 LMTQKTGIVSGFGRTHEKGRQSKVLKMMEVPYVDRNTCRLSTSFSITQNMFCAGYDAKQE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TLVAEXHVLTAAHCIHDGKTYVKGTQK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 LRVGFLKPKFKDGGRGAND---STSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------HDYGKEADDIYVLPAVSPSQELFGKIKVKEVRYLKEFRNLNSKD-AREYD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 YALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRF-----CDVKDE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 TYD---LLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 LSDDGMFLDYQVDTLEGSSGSTVY-----DASHRVVGVHT-----LGDGANQINS 201
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:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                choline binding protein G, truncation [imported] - Streptococcus pneumoniae C; Species: Streptococcus pneumoniae C; Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTLVAEXHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKF
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23.8%; Pred. No. 0.0043;
iive 30; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 DFLLNYPFSTSVKLSTGCTG----
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Best Local Similarity
Matches 58; Conserv
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Gene: cbpG-truncation
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Best Local S
Matches 57
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Gaps

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A; Molecule type: mRNA
A; Residues: 19-284, E', 289-488 < KAU>
A; Residues: 19-284, E', 289-488 < KAU>
A; Residues: 19-284, E', 289-488 < KAU>
A; Residues: 19-284, E', 19-213; NID: 19-213; PIDN: AAAS1984.1; PID: 19-1336
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A; Title: Characterization of an almost full-length cDNA coding for human blood coagulatic
A; Reference number: A22208; MUID: 85216545; PMID: 2582420
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A;Residues 1.488 kMES.
A;Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
A;Cross-references: GB:M57285; NID:g182389; PIDN:AAA52421.1; PID:g182390
R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
A; Biol. Chem. 267, 7395-7401, 1992
A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagula
A;Reference number: A42485; MUID:92218390; PMID:1313796
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A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weinst
Biochemistry 22, 2875-2884, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 1.5-Nov-1994 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A005
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Bichemierry 25, 5098-510, 1986
A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is earlier or number: A24478; MUID:87026600; PMID:3768336
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A; Residues: 1-488 <LEX.
A; Residues: 1-488 <LEX.
A; Crossier. Ferences: UNIPROT:P00742; GB:L29433; GB:M14327; NID:g459809; PIDN:AAA52764.1; I
R; Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A; Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagn
A; Reference number: JQ0917; WUID:91216473; PMID:1902434
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A;Residues: 1-15 <MLA>
A;Residues: 1-15 <MLA>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIP:93787)
B;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
R;Kaul, 1311-314, 1986
A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A;Reference number: A25853; MUID:86221713; PMID:3011603
    199 FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
                                                 --QYVSVQKIVVHPYW---NSDNVAAGYDIALLRLAQSVTL 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human N;Alternate names: Stuart factor
                                                                             ----SQNDGTE---
                                                                                                                                                                                                                                     133 NSYVQLGVLP 142
                                                                                                                                                           258 RKFMKIGVSP 267
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A;Residues: 41-179 <MCM>
R;Inoue, K.; Morita, T.
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C;Date: 03.Aug-1998 #sequence_revision 03.Aug-1998 #text_change 28-Apr-2003
C;Accession: 870439
R;Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
NA Seq. 2, 303-312, 1992
A;Title: Genomic organization of the human homologue of the rat pancreatic elastase I ge
A;Reference number: A56615; MUID:92338395; PMID:1633328
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A; Molecule type: DNA

A; Molecule type: NA

A; Cross-treferences: 1-267 «KM».

A; Cross-treferences: ENBL:X62259; NID:931246; EMBL:X62258; GB:S40923; NID:931247; EMBL:X6

5; GB:S40856; NID:931251; EMBL:X62256; GB:S40857; NID:931252; EMBL:X62257; GB:S40859; NI

5; GB:S40856; NID:931251; EMBL:X62256; GB:S40857; NID:93125; EMBL:X62257; GB:S40859; NI

C; Comment: This apparently silent human homolog of pancreatic elastase I is a single-cogunctional protein in some other tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
    --- TNGAVPDVLQQGRLLVVDYATCSSSAWW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 NYPFSTSVKLSTG-----CTGTLVAEXHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 NYPFSTSVKLSTG-----CTGTLVAEXHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Gaps
                                                                                                                                                                                                                                                                                                                                                        pancreatic elastase I (allele HEL1-16) probable splice form I - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.4%; Score 114; DB 4; Length 258; Best Local Similarity 26.9%; Pred. No. 0.037; Matches 35; Conservative 23; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%; Score 114; DB 4; Length 267; 26.9%; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: S70439
A,Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-258 «KAW»
A;Note: it is not known whethere the gene is expressed
F;19-251/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 12
C;Keywords: hydrolase; pseudogene; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Mismatches
                                                                             ---IKGNYLDCREGDTV 386
                                                                                                                                                       193 GSSVKTSMI-CAGGDGV 208
--YPCYVTGWGRLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 -----SQNDGTE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::::|| |
124 NSYVQLGVLP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 RKFMKIGVSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 35; Conserv
                                                                             373
153
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1129-164/Domain: EGF homology < EG2>
1183-486/Product: coagulation factor X heavy chain #status experimental <APT>
1183-234/Domain: activation peptide #status experimental <APT>
1235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
1225-486/Product: coagulation factor Xa heavy chain #status experimental <ACT>
1225-462/Domain: trypsin homology <TRY>
146.47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #station factor is activated predicted
150-101,95-110,112-121,129-140,136-149,151-164,172-342,241,246,261-277,390-401,15-443/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ritle: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
Reference number: A49458; MUID:93360277; PMID:835579
Contents: annotation; X-ray crystallography, 2.2 angstroms
comment: The two chains held together by one disulfide bond are formed from a single-comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peethway: blood coagulation.
Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology;
Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam;
1-23/Domain: signal sequence #status predicted <SIG>
124-40/Domain: propeptide #status predicted <PRO>
125-84/Domain: Gla domain homology <GLA>
141-179/Product: coagulation factor X light chain #status experimental <LCH>
190-121/Domain: EGF homology <EGL>
190-121/Domain: ACF homology <EGL>
190-121/Domain: EGF homology <EGL>
190-121/Domain: ACF homology <EGL>
190-121/Domain: EGF homology <EGL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bla
                                                                                                                                                                                                                                                                                                                                                                                    A; Note: identification and characterization of beta-hydroxyaspartic acid
R; Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, G.
Gene 84, 517-519, 1989
A; Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A; Reference number: I54051; MUD: 90128299; PMID: 2612918
A; Accession: I54051
A; Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #stat
Eur. J. Blochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides
A;Reference number: S39414; MUID:94062825; PMID:8243461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330; Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Mol. Biol. 232, 947-966, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental
721,231/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- ETYDLLYQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YGVYVRMWKRQQQKWERKIIGI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 LMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDT--K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 CTGTLVAEXHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----brolavlriktpit---FRMNVAPACLPERDWAEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 QWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.4%; Score 114; DB 1; Length 488; 20.9%; Pred. No. 0.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 --KQLPG-----GRIHFSGYDNDRPGNLVYRFCDVKD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Map position: 13g34-13g34
Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
Note: deficiency of this factor causes Stuart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GDB:119890; OMIM:227600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 20.9% hes 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 QCDAQPGASG----
                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 183-234 <INO>
A,Note: glycosylation sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-23 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: GDB:F10
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Best Local S
Matches 57
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 183-295, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <TJ
A; Rote: Carbohydrate binding sites and disulfide bonds were determined
R; Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A; Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal & A; Reference number: A34412; MUID: 89380326; PMID: 2789221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
B; Molecule type: protein
B; Molecule type: protein
B; Molecule type: protein to the molecule type: protein 
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A; Sugo, T.; Bjork, I.; Hablagran, A.; Stenflo, J.

J. Biol. Chem. 259, 5705-5710, 1984

A; Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic

A; Cantentes number: A38024; MUID:84185716; PMID:6546930

A; Contente: annotation; calcium binding

R; Morita, T.; Jackson, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr.1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C;Date: 24-Apr.1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C;Date: 24-Apr.1984 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
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Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing & A;Reference number: A22867; MUID:84247315; PMID:6330671
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A; Realdues: 41-102, N', 104-180 < ENF>
A; Realdues: 41-102, N', 104-180 < ENF>
Biochem: B.A.; Fujikawa, K.; Kisiel, W.
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A; Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood of A; Reference number: A20274; MUID: 83308813; PMID: 668856
A; Contents: annotation; revision to residue 103
B; Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad Sci. U.S.A. 72, 3082-3086, 1975
A; Title: Sovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A; Reference number: A12030; MUID: 76053069; PMID: 1059093
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Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides
A;Reference number: S39414; MUID:94062825; PMID:8243461
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A; Cross-references: UNIPROT: P00743; GB: X00673; NID: g192; PIDN: CAA55286.1; PID: g193
R; Enfield, D.L.; Exicason, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A; Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A; Reference number: A14997; MUID: 80130563; PMID: 6766735
                                                                                                                                                                                                                                                                                                                                                                                                                coagulation factor Xa (EC 3.4.21.6) precursor - bovine N;Alternate names: Stuart factor
: :|:| : :|| 456 TAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK
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A,Residues: 85-126 <PER>
A,Note: beta-hydroxyaspartic acid site
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A,Cross-references: UNIPROT:P08419; GB:M16651; NID:g164441; PIDN:AAA31027.1; PID:g164442 C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; serine proteinage C;Keywords: hydrolase; serine proteinage F;1-16,Domain: signal sequence #status predicted <SIG> F;1-28/Domain: signal sequence #status predicted <PRO> F;2-26/Domain: propeptide #status predicted <MAT> F;2-26/Domain: trypsin homology <TRY> F;29-26/Domain: trypsin homology <TRY> F;73,121,216/Active site: His, Asp, Ser #status predicted
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R;Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 3307-3330, 1986
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II
A;Reference number: A93646; MUD:87066713; PMID:3641189
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A;Accession: A2528
A;Residues: 1-271 <STE>
A;Residues: 1-271 <STE>
A;Cross-references: UNIPROT:P05208; GB:X04573; NID:g50825; PIDN:CAA28242.1; PID:g50826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : 
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Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 TY--VKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 TYRVVLGRHSL------STNEPGSLA------VKVSKLVVHQDW---NSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 RQIYGYDSRFSIFGKDFLLNYPFSTSVKL-STG-----CTGTLVAEXHVLTAAHCIHDGK
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$31-21/Product: parcredite elastase II #status predicted
F;31-264/Domain: trypsin homology <TRY>
F;75,123,218/Active site: His, Asp, Ser #status predicted
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                                                      A; Molecule type: mRNA
A; Residues: 1-269 < KAW>
                A; Accession: A26823
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R;Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
A;Title: Characterization of pancreatic elastase II CDNAs: two elastase II mRNAs are exp
A;Reference number: A90958; MUID:87217962; PMID:3646943
                                                                                                                                                                                                                                                                                                                                                                      Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strd
Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
                                                                                                                                                        Comment: Factor Xa converts prothrombin to thrombin during blood clotting. Comment: The two chains are formed from a single-chain precursor by the excision of to Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: catalyzes the proteolytic activation of prothrombin to thrombin in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 DACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGK--FGVYTKV--SNFLKWIDKIMKA 467
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N,Alternate names: pancreatopeptidase B
C;Species: Sus scrofa domestica (domestic pig)
C,Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 CGGTILNEFYVLTAAHCLHQAKRFT-----VRVGDRNTEQEEGNEMAHEVEMTV-KHSRF
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J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800
A;Contents: annotation; sulfate binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 ---QLPG----GRIH------
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                                                                                                                                                                                                                                                                                                                           activation.
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A;Residues: 1-125,'G',127-183,'L',185-266 <TAN>
A;Cross-references: GB:D00160; NID:g217683; PIDN:BAA00118.1; PID:g217684
A;Note: the authors translated the codon GGG for residue 58 as Gln, GGC for residue 126 &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           panceatic elastase (EC 3.4.21.36) I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A00960; A20534
R;MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Rutte:
Biochmaierry 21, 1453-1463, 1982
A;Title: Primary structure of two distinct rat pancreatic preproelastases determined by & A;Reference number: A00960; MUID:82182967; PMID:6918221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P00773; GB:V01234; NID:g56088; PIDN:CAA24544.1; PID:g56089
                                                                                                                                                                                                                                                                                                                                                                       A; Modecule type: protein
A; Modecule type: protein
A; Residues: 27-91, NV, 99-203, NV, 205-266 <SHO>
A; Residues: 27-91, NV, 99-203, NV, 205-266 <SHO>
R; Shotton, D.M.; Hartley, B.S.
Nature 225, 811-816, 1970
A; Title: Three-dimensional structure of tosyl-elastase.
A; Reference number: A93160; MOID: 70114044; PMID: 5415110
A; Contents: annotation; Kray crystallography, 3.5 angstroms; active site C; Superfamily: trypsin; trypsin homology representance; zymogen
C; Superfamily: trypsin; trypsin homology represents zymogen
F; 1-16/Domain: signal sequence #status predicted <&IGS
F; 17-26/Domain: activation peptide #status predicted <&RFT>
F; 17-25/Domain: trypsin homology crry>
F; 25-25/Domain: trypsin homology crry>
F; 25-25/Domain: trypsin homology crry>
F; 25-25/Domain: trypsin homology crry>
F; 27-115, 223-220, 184-200, 210-240/Disulfide bonds: #status experimental
F; 71, 119, 214/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 NYPESTSVKLSTG-----CTGTLVAEXHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rishotton, D.M.; Hartley, B.S.
Biochem. J. 131, 643-675, 1973
A.Fitle: Evidence for the amino acid sequence of porcine pancreatic elastase.
A.Reference number: A90267; MUID:73229121; PMID:4578945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Isolation and characterization of rat pancreatic elastase A,Reference number: A20534; MUID:84000385; PMID:6555050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.3%; Score 112; DB 1; Length 266; Best Local Similarity 27.3%; Pred. No. 0.057; Matches 36; Conservative 21; Mismatches 41; Indels
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A; Molecule type: protein
A; Residues: 17-37, X', 39-45 < LAR>
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
E; 11-16/Domain: signal sequence #status predicted <SIG>F; 17-26/Domain: activation peptide #status predicted <APT>F; 27-26/Product: elastase I #status predicted <APT>F; 27-256/Product: trypsin homology <TRY>F; 27-259/Domain: trypsin homology <TRY>F; 21, 119, 214/Active site: His, Asp, Ser #status predicted
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Biochemistry 22, 3763-3770, 1983
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132 NSYVQLGVLPRA 143
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Best Local Similarity
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A;Residues: 1-266 <MAC>
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R; Readdues: 37-95,98-259 «OLA»

R; Readdues: 37-95,98-259 «OLA»

B; Readd. N.J.; James, M.N.G.

J. Mol. Biol. 200, 523, 1988

A; Title: Refined crystal structure of Streptomyces griseus trypsin at 1.7 angstroms resc

A; Reference number: A4-87-4; MUID: 8828673; PMID: 3135412

A; Contents: annotation; X-ray crystallography, 1.7 angstroms

A; Note: residues 96-97 modeled as Gly-Ala
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A;Residues: 1-266 cSHI:
A;Cross-references: UNIPROT:P00772; GB:X04036; GB:D00070; GB:N00070; NID:g1941; PIDN:CAA
A;Cross-references: UNIPROT:P1: A: Ohmine, T.; Takiguchi, Y.
J. Biochem. 101, 591-599, 1987
J. Biochem. 101, 591-599, 1987
A;Title: Characterization of a silent gene for human pancreatic elastase I: structure of
A;Reference number: A26777; MUID:87250343; PMID:3648024
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:P00775; GB:M64471; Axperimental source: strain ATCC10137; Alason, R.W.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B. dochemistry 14, 1168-1177, 1975; Alitle: Amino acid sequence of Streptomyces griseus trypsin. Cyanogen bromide fragments; Reference number: A00962; MUID:75127940; PMID:804314
                          C;Species: Streptomyces griseus
C;Date: 24-Apr-1984 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Datession: JQ1302; A00962
R;Kim, J.C.; Cha, S.H.; Jeong, S.T.; Oh, S.K.; Byun, S.M.
Blochem. Biophys. Res. Commun. 181, 707-713, 1991
A;Title: Molecular cloning and nucleotide sequence of Streptomyces griseus trypsin gene.
A;Reference number: JQ1302; MUID:92095977; PMID:1755852
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence.revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0013; A26777; A10061; A00959
R;Shirasu, Y.; Yoshida, H.; Mikayama, T.; Matsuki, S.; Tanaka, J.I.; Ikenaga, H.
A;Title: Isolation and expression in Escherichia coli of a cDNA clone encoding porcine A;Reference number: A92005; MUID:86304235; PMID:3528137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 DS---TSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
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Cikeywords: hydrolase; serine proteinase
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-36/Domain: propeptide #status predicted <PRO>
F;37-256/Product: trypsin #status experimental <NAT>
F;37-252/Domain: trypsin homology <TRY>
F;38-74,177-192,204-233/Disulfide bonds: #status experimental
F;33,118,208/Active site: His, Asp, Ser #status experimental
trypsin (EC 3.4.21.4) precursor - Streptomyces griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 5.3%; Score 112.5; DB 1; Local Similarity 26.0%; Pred. No. 0.05; nes 39; Conservative 21; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TTTAYNQ---GTFTVAGWGANREGGSQQRY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 VSPPAKQLPGGRIHFSGYDNDRPGNLVYRF 294
                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-259 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: A00962
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Search completed: July 1, 2005, 21:09:18 Job time : 24.826 sec8
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A;Molecule type: DNA
A;Residues: 1-522 <WAT>-
A;Residues: 1-522 <WAT>-
A;Cross-references: UNIPROT:001771; EMBL:AF003134; PIDN:AAB54144.1; GSPDB:GN00019; CESP:A;Experimental source: strain Bristol N2; clone ZC581
  7;
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                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZCSB1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T29767
R;Waterston, B.; Gattung, S.; Le, T.T.
R;Waterston, B.; Gattung, S.; Le, T.T.
A;Description: The sequence of C. elegans cosmid ZCSB1.
A;Reference number: Z2062
A;Accession: T29767
                                                                             26 RVVGGAEARRNSWPSQISLQY-----LSGGSWYHTCGGTLIRRNWVMTAAHCVSSQMT
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Best Local Similarity 20.6%; Pred. No. 0.13;
Matches 95; Conservative 53; Mismatches 160; Indels 154; Gaps
48; Indels 36; Gaps
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A;Introns: 36/2; 138/3; 234/2; 311/1; 331/1; 421/1; 470/2
  23; Mismatches
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07ngb4
09jj88
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06azc0
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09qx90
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9NJS5	FA10_RAT	Q81HL5	Q8DR41	FA10 HOPST	Q9XY <u>6</u> 1	046644	Q6UWB4	Q9EXR9	FA10 RABIT	Q90WF9	Q61CV2	Qeisus	Q91WP0
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046644 06UWB4 09UWB4 09UWF9 090WF9 06ISU5 091WP0	ALIGNMENTS ALIGNMENTS PRT; 383	nence u otation SC 3.4.	; Catarrhini ; Catarrhini	from human umbilical the EMBL/GenBank/DDBJ	linek L., Foa SMBL/GenBank,	uther R., Garker H., Baue Bayer A., Kod Obermaier E., Poustka A., Benes and present of the protein control of the	73199; DOI=10 7a E., Baker. C., Gu Q., C., Gu Q., C., Gu Q., C., Smith M., Smith M., Zhang Z M., Zhang Z M., Zhang Z M., Zhang Z
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carahnor T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield W., Schein J.E., Jones S.J.M., Marra M.A.,
Brid M., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@lsb-sib.ch).
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Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
N-linked (GlCNAc. ..) (Potential).
N-linked (GLNAc. ..) (Potential).
                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.8%; Score 2044; DB 1; Length 383; 98.4%; Pred. No. 9.1e-173; ive 1; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the peptidase S1 family.
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H-InvDB; HIX0010006; -..
H-InvDB; HIX0010006; -..
InterPro; IPR009003; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
PR0175; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; FALSE_NEG.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
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Best Local Similarity 98.4*
Matches 377; Conservative
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175
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316
176
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240 2
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 SEQUENCE FROM N.A.
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TISSUBLICE FROM N.A.

TISSUB-Kidney;

Director MGC Project;

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

Li SIMILARITY: Belongs to peptidase family S1.

-1- SIMILARITY: Belongs to peptidase family S1.

RML; BC079219; AAH79179.1. -.

RR GO; GO:0000786; C:nucleus; IEA.

GO; GO:0000786; C:nucleus; IEA.

RG; GO:0000787; F:DNA binding; IEA.

RG; GO:00007001; P:DNA binding; IEA.

RG; GO:0006534; P:nucleosome assembly; IEA.

RG; GO:0006508; P:proteolysis and peptidolysis; IEA.

RG; GO:0006508; P:proteolysis and peptidolysis; IEA.

RITHEFPC; IPR001951; Histone H4.

RITHEFPC; IPR001554; Peptidase_S1.
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SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
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                                                                                       KTYVKGTOKLRVGFLKPKPKDGGRGANDSTSAMPEOMKFOWIRVKRTHVPKGWIKGNAND
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                                                                                                                                                                                                                   IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
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ACT_SITE
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CARBOHYD
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STRAIN=C57BL/6J; TISSUE=Tongue;

STRAIN=C57BL/6J; TISSUE=Tongue;

KN MBDLINE=213546813; PubMed=1246881; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbach J.,

Schrimi L.M., Kanapin A., Matsuda H., Batalov S., Balsel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Gariboldi M., Gissi C., Godzik A., Grayh J.,

Grammond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B. L., Lyons B.L.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
                                                                                                                                                                                      241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                      1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                                                                                                                                                                                                          VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS
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                                                                                                                                               Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                   DB 2; Length 383;
                                  PRINTS; PR00722; CHYMOTRYPSIN.
PRODOM; PD001827; Histone H4; 1.
PROSITE; PS00134; TRYPSIN—HIS; UNKNOWN 1.
Hydrolase; Hypothetical protein; Protease; Serine protease.
SEQUENCE 383 AA; 43159 WW; 4AB12CC7B66CDFC8 CRC64;
                                                                                                                                            26; Indels
                                                                                                                Query Match

89.1%; Score 1881; DB 2;
Best Local Similarity 90.3%; Pred. No. 2.6e-158;
Matches 346; Conservative 11; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS23 MOUSE STANDARD; PRT; 382 AA. Q9D6X6, Q8VEC1; Treated) 28-FBB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Serine protease 23 precursor (EC 3.4.21.-).
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InterPro; IPR001314; Peptidase_S1A
         InterPro, IPR009003; Pept_Ser_Cys.
Pfam; PF00089; Trypsin; 1.
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TISSUE=Breast tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSDERG R.L., Feligodd E.A., Grouse L.H., Derge J.G.,

METALINE R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MARCHAR R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Myllalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raheto J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Modriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
Sandelin A., Schneider C., Semple C. R., Secou M., Shimada K., Sultana R., Takenakar Y., Taylor M.S., Teasdale R.D., Tomita M., Sultana R., Takenakar Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wanshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yang L.,
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Proc. Natl. Acad. Sci. U. SA. 99:16899-16903(2002).
-i- SUBCELLULAR LOCATION: Secreted (Potential).
-i- SIMILARITY: Belongs to the peptidase SI family.
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N-linked (GlcNAc.
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InterPro; IPR001254; Pept Ser Cye.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
PENTS; PR00132; CHYMOTRYPSIN.
SMART; SMO0202; TYPS SRC; I.
PROSITE; PS001030; TRYPSIN DOM; FALSE NEG-PROSITE; PS00134; TRYPSIN LIS; 1.
PROSITE; PS00135; TRYPSIN SER; FALSE NEG-HYDORDAGE; Serine protease; Serine protease; Serine Interpretation.
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                                                                                                                                                                60 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETRVGIYILSNGEGRARGRDSEA 119
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                                                                                                                                                   61 VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS 120
                                                                                                                                                                                                     121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG 180
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Hanalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                    1 MAGIPG-LFILLVLLCVFMQVSPYTVPWKPTWPAYRLPVVLPQSTLNLAKADFDAKAKLE
                                                                                                                                                                                                                                                                                                                    240 IGMDYDYALLELKKPHKRQFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                                                                                                                                     300 TYDLLYQQCDAQPGASGSGVYVRAMKRPQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6J; TISSUB=Cecum; MBDLINE=9927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                    MAGI PGLLFLLFFLLCAVGOVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR_2003 (TrEMBLrel. 23, Created)
01-MAR_2003 (TrEMBLrel. 23, Last sequence update)
01-MAR_2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male eccum cDNA, RIKEN full-length enriched
library, clone:9130215B18 product:SERINE PROTEASE (HYPOTHETICAL 43.0
kDa PROTEIN) (PROTEASE, SERINE, 23) homolog.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
N-linked (GlcNAc. .) (Potential).
M -> I (in Ref. 1; BAB26541).
; 6F09A5C80A5B2306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                           1,
                                                   DB 1; Length 382;
                                                Query Match 88.4%; Score 1866.5; DB 1; Length
Best Local Similarity 89.8%; Pred. No. 5.1e-157;
Matches 344; Conservative 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/61; TISSUE=Cecum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                         360 ITPLKYAQICYWIKGNYLDCREG 382
                                                                                                                                                                                                                                                                                                                                                                                                        361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
206 206 N
260 260 M
382 AA; 43071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                     181
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Q8BZS4;
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RESTRAIN-CSTBL/G1; TISSUB-Cecum;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Ratchia S., Puruno M., Hanagaki T., Hara A., Hashizume W.,

RA Fukuda S., Puruno M., Hanagaki T., Hiraoka T., Hirozane T.,

RA Fach H., Kawai J., Kijima Y., Konno H., Kouda M., Koya S.,

RA Katch H., Kawai J., Kojima Y., Konno H., Rouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Salto R., Saltoh H., Sakai C., Sakazume M., Sapabe Y., Tagami M.,

RA Sasaki D., Shibata K., Shinagawa A., Shazaki Y., Sogabe Y., Tagami M.,

RA Sasaki D., Shibata K., Shinagawa A., Muramatsu M., Hayashizaki Y.,

RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RO Sasaki D., Shibata K., Shinagawa A., Muramatsu M., Hayashizaki Y.,

RO Sasaki D., Shibata K., Shinagawa A., Sharki T., Sogabe Y., Tagami M.,

RO Sasaki D., Shibata K., Shinagawa A., Muramatsu M., Hayashizaki Y.,

RO Sasaki D., Shibata K., Shinagawa A., Sharki Y.,

REMILARITY: Belongs to peptidase family Sl.

-- SIMILARITY: Belongs to peptidase family Sl.

BR G0: G0:0004235; F:chymotrypsin activity; IEA.

G1: G0:0004235; F:trypsin activity; IEA.

BR G0: G0:0004235; F:trypsin activity; IEA.

G2: G0:0004235; F:trypsin activity; IEA.

BR RAINTS; PRO0122; CHYMOTRYPSIN.

BRANTS; PRO0122; CHYMOTRYPSIN.

BRANTS; PRO0123; CHYMOTRYPSIN.

BRANTS; PRO0123; CHYMOTRYPSIN.

BRANTS; PRO0124; PRO0134; Pett Ser Cys.

RWATCHERPO: Hypothetical protein; Processe: Serine protease.

SEQUENCE 382 AA; 43147 MW; 556789818EIZA081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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[4]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Cecum;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu W., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu W., Hayashizaki Y.;
Normalization and subtraction of Cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CS7BL/61; TISSUE-Cecum;
STRAIN=C3030913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
A MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Asmamoto H., Ishihi Y., Makamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A. Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., A. Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Noneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTYVKGTQKLRVGFLKPKYKDGAGGDNSSSSAMPDKMKFQWIRVKRTHVPKGWIKGNAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAGIPG-LFILLVLLCVFMQVSPYTVPWKPTWPAYRLPVVLPQYTLNLAKADFDAKAKLE
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89.6%; Pred. No. 1.7e-156;
.ive 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 89.68
Matches 343, Conservative
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bioinformatics assessment."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad.
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                            Q8N3Z0;
                                                                                                                 Q8N3Z0
                                                                                          RESULT 6
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                                           360
                                                        300 TYDLLYQQCDAQPGASGSGVYVRMWKRPQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 359
300
                      299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 -RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDGKTY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 PAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGYGVYVRMWKR 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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            IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                           TYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLFLLFFLLCAVG--QVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 CGIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLE----PTQNITTKGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 VKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLRERAKGGRRRKKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.7%; Score 1029; DB 2; Length 413; 47.6%; Pred. No. 1.2e-82; ive 65; Mismatches 107; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 VKGTQKLRVGFLKPKFKDGGR------GANDSTSAMPEQMK-
                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to peptidase family S1.
EMBL, A1121939; CAC35071.1; -.
MEROPS; S01.994; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SN00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Procease; Serine procease.
SEQUENCE 413 AA; 47098 MW; 818D9C951BD2D6C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:21387; PRSS35.

GO; GO:0004233; F:chymotrypsin activity; IEA.

GO; GO:0004235; F:chypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001319; Peptidase S1A.

InterPro; IPR009003; Pept. Ser. Cys.

Pfam; PF00089; Trypsin; 1.
                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DJ223E3.1 (Putative secreted protein ZSIG13).
                                                                                         361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                               360 ifplkyağıcywikGNYLDCREG 382
                                                                                                                                                                                               Created)
                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 47.69
Matches 198; Conservative
                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                         Name=dJ223E3.1;
                                           301
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TISSUE=Brain,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratuabberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratuaberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Rother R.E., Jordan H., Moore T., Max S.I., Wang J., Hafeh F.,

Districhench L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotiguez A.C., Galimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Mczywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
298 TIKKMPGGMIHFSGFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLKDP 357
                                                                                                                                                         328 QQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITFLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                              358 DKKNWKRKIIAVYSGHOWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-PRSS35; ÖRFNames-UNG522;
Amo saplens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: Belongs to peptidase family Sl.
EMBL, BC037170.1; --
GO; C0004263; F:chymotrypsin activity; IEA.
GO; GO:0004233; F:chyptidase activity; IEA.
GO; GO:0004235; F:ryptidase activity; IEA.
GO; GO:0006295; F:ryptidase activity; IEA.
GO; GO:0006295; P:ryptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein PRSS35 (ENMLS22).
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                                                                                                                                                                   178 VKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKKSG
                                                                                                                                                                                                                                                                                                                                                         238 RGQRIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISP
                                                                                                                                                                                                                                                                                                                                                                                                                298 TIKKMPGGMIHFSGFDNDRADQLVYRFCSVSDESNDLLYOYCDAESGSTGSGVYLRLKDP
                                                                                                                                                      7 LLFLLFFLLCAVG--QVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSS
                                                                                                                                                                                                   65 CGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGSSGKS
                                                                                                                                                                                                                62 CGIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLE----PTQNITTKGVS
                                                                                                                                                                                                                                                125 -RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDGKTY
                                                                                                                                                                                                                                                            118 VRRKRQVYGTDSRFSILDKRFLTNPPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDY
                                                                                                                                                                                                                                                                                              VKGTQKLRVGFLKPKFKDGGRGANDSTSAMPE---------
                                                                                                                                                                                                                                                                                                                                                                                          PAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGYGVYVRMWKR
                                                                                                                                                                                                                                                                                                                                            -----OMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                              Gaps
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030494122 product:similar to D0223E3.1
(PUTATIVE SECRETED PROTEIN ZSIGI3), full insert sequence (Protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 QQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLDCREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                                                                46;
                                                                                                     48.7%; Score 1028; DB 2; Length 413; 47.6%; Pred. No. 1.4e-82; tive 65; Mismatches 107; Indels 4
                             PROJECT PRODUCT Trypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Hypothetical protein; Protease; Serine protease.
SEQUENCE 413 AA; 47070 MW; 2D438145190305C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J, TISSUE=Testis,
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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01-MAR-2003 (TrEMBLrel. 23, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
       InterPro; IPR001314; Peptidase_S1A
InterPro; IPR009003; Pept_Ser_Cys.
IPR001254; Peptidase
                                                                                                                  Best Local Similarity 47.69
Matches 198; Conservative
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STRAIN=C57BL/6J; TISSUE=Head;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 -GRGA-----KFQWIRVKRTHVPKG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 KRRGSKRSRREAESAGQSQAHLRESTTQRPGKKSRRGPRVTQGRPSFQWTRVKSTHIPKG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 WIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 RFCDVKDETYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSP 352
                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 YANGSRTEXQVGIY1L-----SSSGDGAXXRDSGSSGKSRRKRQIYGYDSRFSIFGKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 LLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                      31 TWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLPTYKEAKQYLSYETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] ____SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                Query Match
47.5%; Score 1003.5; DB 2; Length 409;
Best Local Similarity 48.8%; Pred. No. 2.1e-80;
Matches 191; Conservative 68; Mismatches 85; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 6 days neonate head CDNA, RIKEN full-length
11brary, clone:543041709 product:similar to DJ223E3.1 (P
SECRETED PROTEIN ZSIG13), full insert sequence.
(JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                        PRINTS; PRO072; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 409 AA; 45787 MW; 6E22D4A908E7EFES CRC64;
                  -i- SIMILARITY: Belongs to peptidase family Sl.
EMBL; AK031411; BAC27392.1; -.
EMBL; BC075675; AAH75675.1; -.
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                                                                            MGD; MGI:2444800; Press35.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IRR01254; Peptidase S1.
InterPro; IRR001314; Peptidase S1A.
InterPro; IRR009003; Pept Ser_Cys.
Pfam; PF00089; Trypsin; 1.
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01-MAR-2003 (TrEMBLrel. 23, Created)
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SEQUENCE FROM N.A.
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Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Alzawa K., Akimura T., Hara A., Habhizume W.,
Adachi J., Alzawa K., Akimura T., Hara A., Habhizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Konno H., Kouno H., Kouda M., Koya S.,
A Kurihara C., Maresuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito H., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Togawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

Salla AKOOSTI: Balongs to peptidase family S1.
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STRAIN=C57BL/6J; TISSUE=Head;
X MEDIARE=20350913; PUDMed=11076861; DOI=10.1101/gr.152600;
X Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nishi K., Kitsunai T., Tashiro H., Itoh M., Nonno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Matsuura S., Kawai J., Yoneda Y., Riza A., Hayashizaki Y., Ishikawa T., Gama W., Inoue Y., Kira A., Hayashizaki Y., Ishikawa T., Gama W., Inoue Y., Kira A., Hayashizaki Y., Ishikawa T., Gama W., Inoue W., Inoue W., Ishikawa T., Gama Yasis Gama J., Gama W., Ishikawa T., Calawa W., Ishikawa T., Gama Yasis Gama J., Gama Yasis Gama K., Ishikawa T., Calawa W., Ishikawa T., Calawa Y., Kira A., Hayashizaki Y., Kira W., Ishikawa T., Calawa W., Ishikawa T., Calawa Y., Kira A., Hayashizaki Y., Kira K., Kira M., Ishikawa T., Calawa W., Kira A., Hayashizaki Y., Kira M., Ishikawa T., Calawa W., Kira M., Mayashizaki Y., Kira M., Ishikawa T., Calawa W., Kira M., Mayashizaki Y., Kira M., Kira M., Kira M., Mayashizaki Y., Kira M., Mayashizaki Y., Kira M., Mayashizaki Y., Kira M., Mayashira W., Kira M., Mayashira W., Kira M., Mayashira W., Kira W., Kira M., Mayashira W., Kira W., Mayashira W., Mayashira W., Mayashira W., Kira W., Mayashira W., Kira W., Mayashira W., Kira 
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MEDLINB=2049314; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINB=2049314; PubMed=11042159; DOI=10.1101/gr.145100;
Carno H., Okazaki Y., Hayateu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length control of cap-trapper-selected cDNAs for genes.;
Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLPTYKEAKQYLSYETL
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                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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48.6%; Pred. No. 5.8e-80;
iive 68; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005615; C:extracellular space; TAS
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SMART; SM00020; Tryp, SPC; 1.
PROSITE; PS00134; TRVPSIN HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
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InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM CONSOLTIUM,
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Nature 420:563-573(2002)
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Altausher R. D., Collins F. S., Wagner L. Bharmen C. M., Schuler G. D.,
Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,
Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,
Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,
Burchenko L., Marusina K., Farmer A.A., Rubin G. M., Hong L.,
Stapleton M., Soares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. E.,
Brownstein M. J., Usdin T. B., Tooshiyuki S., Carninci P., Prange C.,
Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,
Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,
Villalon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,
Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C.,
Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M., Butterfield Y. S.,
Krzywinski M. I., Skalska U., Smailus D. E., Schnerch A., Schein J. E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                           318
                                                  202
                                                                 -GRGA-----KFQWIRVKRTHVPKG 232
                                                                                                                                                     292
                                                                                                                                                                                                                  YANGSRIEXQVGIYIL----SSSGDGAXXRDSGSSGKSRRKRQIYGYDSRFSIFGKDF 144
                                                                                                                            199 KRRGSKRSRREAESAGQSQAHLRESTTQRPGKKSRRGPRVTQGRPSFQWTRVKSTHIPKG 258
                                                                                                                                                                                                    RFCDVKDETYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSP 352
                                                                                                                                                                  PENGTRILIRVKVQGLVLEPTRNSSVKGA-------HPRRRRQVYGTDSRFSILDKRF
                                                 LLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDG--
                                                                                                                                                   WIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Whole;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                    379 KDYNEAVRITPLKYAQICLWIHGNAANCAYG 409
                                                                                                                                                                                                                                                    353 QDFNVAVRITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                                                                                                                                                                                                  OKFNames=zgc:91804;
Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                              61 VSSSCGPQCHKGTPLPTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LHGICGIECOORLPEPSLDDLEQLLSYETMYDNGTRTLTTVTVQDLNVSNDWT----GAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEXHVLTAAHCIHDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 GGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 KIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGYGVY
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STRAIN-CS7BL/64; IISSUE-Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
(Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:603046M24 product:similar to DJ223E3.1
(PUTATIVE SECRETED PROTEIN ZSIG13), full insert sequence.
                                                                                                                                                                                                                                                43;
                                                                                                                                                                                          Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
InterPro; IPR001254; Peptidase S1.
InterPro; IPR009003; Pept_Ser_Gys.
Pfam; PF00089; Trypsin, 1.
PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
Hydrolase; Protease; Serine protease.
SEQUENCE 418 AA; 47270 MW; AF53345CEE94F720 CRC64;
                                                                                                                                                                                          47.1%; Score 994.5; DB 2; 45.8%; Pred. No. 1.3e-79;
                                                                                                                                                                                                               Pred. No. 1.3e-79;
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                                                                                                                                                                                                                       Sest Local Similarity 45.04
Matches 193; Conservative
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Nature 409:685-690(2001).
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01-OCT-1993
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashidae W., Puruon M., Hanagaki T., Hara A., Hashidae W., Hayashida K., Hayatsu W., Hiracka T., Hirozane T., Hayashida K., Hayatsu W., Hiracka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kacho H., Kawai J., Kojima Y., Konno H., Shibata K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Sasaki C., Sakai K., Sakazume N., Sano H., Sasaki C., Sakai K., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Rubi M., Ako31644; BAC274911; — EMBL/GenBank/DDBJ databases.

EMBL; AK031644; BAC274911; — EMBL/GenBank/DDBJ databases.

Roc; Go: 0005615; C:extracellular space; TAS.

Richerpo; IPR001254; Peptidase S1.

Richerpo; IPR001254; Peptidase S1.

Richerpo; IPR001254; Peptidase S1.

Richerpo; PR001254; Peptidase S1.
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             SEQUENCE FROM N.A.
STRAIN-CS7BL/GJ; TISSUE-Testis;
The FANTOM CONSORTING SEQUENCY
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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                                                                                                                                                         STRAIN=C57BL/6J; TISSUB=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazadi Y., Muramatsu M., Hayashizaki Y., Nuramatsu M., Hayashizaki Y., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MEDLINE-57BL/64; TISSUE-Testis;
MEDLINE-2650913; Pubmed=11076861; DOI=10.1101/gr.152600;
MEDLINE-26530913; Pubmed=11076861; DOI=10.1101/gr.152600;
Sonio H., Aixyama J., Nalahi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RIKEN integrated sequence analysis (RISA) system-384-format
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48.3%; Pred. No. 2e-79;
iive 70; Mismatches 85;
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Matches 189; Conserv
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                                                                       292
199 KRRGSKRSRREAESAGOSQAHLRESTTQRPGKKSRRGPRVTQGRPSFQWTRVKSTHIPKG 258
                                                                                                                                                                                                                                                                     293 RFCDVKDETYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSP 352
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MEDLINE=3905477; PubMed=1429718;

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Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N.;

"Purification, characterization, cloning, and expression of a glutamic

acid-specific protease from Bacillus licheniformis ATCC 14580.";

J. Biol. Chem. 267:22782-23788[1992]
                                                                       WIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY
                                                                                                                                              259 WVRGENGGLALDYDYALLELKRAHKQQHMELGVSPTITKLPGGQIHFSGFDNDRDEQLVY
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the peptidase S1B family.
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InterPro; IPR001254; Pept Ser_Cys.
InterPro; IPR001254; Pept Gase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001255; Peptidase_S1B.
Pfam; PF00089; Tryp.Sp. Peptidase_S1B.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp.Sp. SPc; 1.
PROSITE; PS00672; V8 HIS; 1.
PROSITE; PS00673; V8_ERR; 1.
Direct protein sequencing; Hydrolase; Serine protease; Signal.
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Svendsen I., Breddam K.;
"Isolation and amino acid sequence of a glutamic acid specific
endopeptidase from Bacillus licheniformis.";
Eur. J. Blochem. 204:165-171(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus licheniformis.
Bacceria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1402;
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Glutamyl endopeptidase precursor (EC 3.4.21.19)
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Hydrolase

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175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SSGKSRRK------RQIYGYDSRFSIFGKDFLLNYPFSTSVKLST---GCTGTLVAE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |: | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:877-877(2004). EMBL; AEO17333; AAU39298.1; -... EMBL; CP000002; AAU21945.1; -...
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Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J. Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B. Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
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                                                                                             Glutamyl endopeptidase.
Charge relay system (By similarity)
Charge relay system (By similarity)
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Ehrenreich A., Gottschalk G.;

"The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential.";

J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.8%; Score 185; DB 1; Length 31 Best Local Similarity 23.2%; Pred. No. 6.4e-08; Matches 77; Conservative 46; Mismatches 139; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
About 1000 (TrEMBLrel. 28, Last annotation update)
Mpr (EC 3.4.21.19) (Glutamyl Endo peptidase).
Mame-ampr; ORFNames=BLO1804, BLi00340;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillase,
                                                                                                                                                                                                                                                                                                                                          33611 MW; 96D7552CB7089B09 CRC64;
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    Potential.
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316 AA;
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SIGNAL
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CHAIN
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                                                                                                                                          63 SSCGPOCHKGTPL---PTYKEAKQYLSYETLYANGSRTEXQVGIYILSSSGDGAXXRDSG 119
                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                176 YFIPSGWRSGNTN----YDYGAIELSEPIGNTVGYFGYSYTTSSLVGTTVTISGYPGDK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 PGNLVYRFCD--VKDETYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKII----GIF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 TAGTQWQHSGPIAISETYKLQYAM-DTYGGQSGSPVFEQSSSRTNCSGPCSLAVHTNGVY 289
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                                                                                                                                                                    28 AQAAPSPH--TPVSSDPSYK-AETSVTYDP-----NIKSDQYGLYSKAFTGTG---KVNE
                                                                                                                                                                                                                            120 SSGKSRRK------RQIYGYDSRFSIFGKDFLLNYPFSTSVKLST---GCTGTLVAE
                                                                                                                                                                                                                                                   : |: | : | | | | : | | | | : | | | 17 TKEKAEKKSPAKAPYSIKSVIGSDDRTRVIN---TTAYPYRAIVHISSSIGSCTGWMIGP
                                                                                                                                                                                                                                                                                                                                227 THVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDR
                                                                                                                                                                                                                                                                                                           168 XHVLTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKR
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15115801; DOI=10.1093/nar/gkh562; Navel J., DeBoy R.T., Rolfon K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T., Kolonay J.F., Rake D.A., Angluoli S.F., Gill S.R., Paulsen I.T., Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J., Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R., Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N., Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A., Bayles D.O., Luchansky J.B., Fraser C.M.; Whole genome comparisons of serotype 4b and 1/2a strains of the food borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species.";
                                                                                                    70;
                                                         Length 316;
                                                         8.8%; Score 185; DB 2; Length 316
23.2%; Pred. No. 6.4e-08;
ative 46; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease, putative.
OrderediocusNames=LMOF2365 1900;
Listeria monocytogenes (Berotype 4b / strain F2365)
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IRR001254; Peptidase S1.
InterPro; IRR001254; Peptidase S1.
InterPro; IRR009003; Peptidase S1B.
InterPro; IRR009003; Pept_Ser_Cys.
Pfam; PF07538; ChW; 3.
SMART; SM00728; ChW; 3.
SMART; SM00728; ChW; 3.
PROSITE; PS01014; TRYPSIN DOM; 1.
Complete proteome; Hydrolase; Protease; Serine protease.
SEQUENCE 450 AA; 48793 MW; 54C79A67510FAD4A CRC64;
                     316 AA; 33611 MW; 96D7552CB7089B09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AE017328; AAT04669.1; -.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 SGHQWVDMNGSPQDFNVAVRITPLKYAQICYW 372
                                                                                                  77; Conservative
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                                                                               Local Similarity
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                     SEQUENCE
                                                           Query Match
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272 GDFTANLVGYPGDKPMGTMWKASCEVHAENIAPEYFQYDCDTFPGSSGSSVYAYDTKSKQ 331
       169 YGSCSATLIGPRTVLTAAHCLYSHEDKDWL--SEYLFV-------PGLNGSTA--- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 KQ----LPGGR-IHFSGYDNDRPGNLVYRFCDVKDE-TYDLLYQQCDAQPGASGYGVYVR 323
                                                                       273 PGGRIHFSGYDNDRP-GNLVYRFCDVKDETYDLLYQQ--CDAQPGASGYGVYVRMWKRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Makazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 TGCTGTLVAEXHVLTAAHCIHDGKTYVKGTQKLRVGF-LKPKFKDGGRGANDSTSAMPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 TGCTAFLISPTRLLTAAHCITSPIRQRLGLPNLAVRIRVTP-----GRASRD---ARP--
                                             215 EQMKFQWIRVKRTHVPKGWIKGNANDIG--MDYDYALLELKKPHKRKFMKIGVSPPAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 MKFQWIRVKRTHV-----PKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPA
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                                                                                                                                                                                                 330 QKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNY 377
                                                                                                                                                                                                                           332 R-----IITG---VNVAESP-DANTAVRLN----AANVQWINSLY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 7.4%; Score 156; DB 2; Length 271; Local Similarity 29.0%; Pred. No. 2e-05; hes 67; Conservative 21; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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PRINTS; PRO0032; CHYMOTRYPSIN.
PRINTS; PRO0039; VBPOTRASE.
SMART; SMO0030; Tryp. SPC; 1.
PROSITE; PS50240; TRŸPSIN_DOM; 1.
COMDIECE PROCOCCOMDIECE SECTION TRYPSIN_HIS; UNKNOWN 1.
COMDIECE 271 AA; 30385 MM; 37659307C63D099C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SIMILARITY: Belongs to peptidase family S1.
EMBL, AP003010; BAB53084.1.; -
OS, GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:crypsin activity; IEA.
GO; GO:0006508; P:proteolygis and peptidolysis; IEA.
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Last annotation update)
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InterPro; IPR001314; Peptidase SIA.
InterPro; IPR008256; Peptidase SIB.
InterPro; IPR009003; Pept_Ser_Cys.
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(TrEMBLrel. 18, 1
(TrEMBLrel. 26, 1
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DNA Res. 7:331-338(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MAFF303099;
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01-OCT-2001
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                                             13;
                                                                               176
                                                                                                       177 IHDGKTYVKGTQKLRVGFLKPKPKDGG------RGANDSTSAMPBQMKFQWIRVKRTH 228
                                                                                                                                                                                                 181
                                                                                                                                                                                                                                     229 VPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKOLPGGRIHFSGYDNDRPG 288
                                                                                                                                                                                                                                                                         182 VPKEWTKKEPS----TEDYGVIKLDKNIGTKTGTMGLTTNT----SGAITISGYHGDKKG 233
                                                                                                                                                                                                                                                                                                               289 NLVYRFCDVKDETYDLLYQQCDAQPGASGYGVYVRMWKRQQQKWERKIIGIFSGHQWVDM 348
                                                                                                                                                                                                                                                                                                                                       234 KLYTQTGNISQVTANNVFYRLDTTGGSSGSGVY-----NSKKQ1LAV-NAYEYLNG 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 ANGADGAERKTEDPGLGEGEAGROVFGPDDREQVRNTK---TYPFSAIGYLEAKSAKTGS 168
                                                                             128 RQIYGYDSRFSIFGKDFLLN---YPFSTS----VKLSTGCT----GTLVAEXHVLTAAHC
                                                                                                                                                                                               147 LY-GK------KAPFGTAKARKYTVYPGYNGT-----KAPFGTAKARKMY
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                                         72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
       DB 2; Length 450;
 8.6%; Score 182; DB 2; Length 45
25.6%; Pred. No. 1.8e-07;
ive 43; Mismatches 86; Indels
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SMART; SMOOD20; Tryp SPc; 1.
PROSITE; PSO0134; TRYPSIN HIS; UNKNOWN 1.
Complete proceemes, Hydrolase; Protease; Serine protease.
SEQUENCE 364 AA; 39034 MW; 13BE653270E7CDD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 7:331-338(2000).

EMBL; AP003001; BAB50229.1; -.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006509; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR008256; Peptidase S1B.

InterPro; IPR009003; Pept. Ser_Cys.
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                                                                                                                                                                                                                                                                                                                                                                                         349 NGSPQDFNVAVRITPLKYAQICYWIKGNYL 378
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01-0CT-2001 (TrEMBLrel. 18, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
Glutamyl endopeptidase (EC 3.4.21.19)
OrderedLocusNames=ml13306;
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                                         Conservative
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Best Local Similarity 26,77
Matches 77; Conservative
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Query Match
Best Local Similarity
Matches 69; Conserv
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ALIGNMENTS

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Copyright (c) 1993 - 2005 Compugen Ltd
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length: 2000000000
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Maximum DB 8
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Sequence:

Run on:

Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp1990s:* geneseqp1990s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003bs:* geneseqp2003bs:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

Aab48973 Human Z81 Aab48972 Human Z81 Aay08657 Human TAN Aay08657 Human TAN Aay88277 Human TAN Aay88277 Human B1G Aay82552 A bone ma Aab25618 Protein e Aab25592 Protein e Aab25592 Protein e Aab25594 Human R80 Aab48974 Human R80 Abu84287 Human R80 Abu87972 Novel hum Abu87972 Human sec Abr65551 Human sec Abu82730 Human sec Abu82730 Human sec Abu82731 Human sec Human PRO Human PRO Human PRO Human PRO Human PRO Novel hum Human sec Description SUMMARIES AAB25618 AAB25592 ADC78573 AAB80258 AAB48974 ABU89851 ABU71491 ABR68100 AAB48973 AAB48972 AAU29048 ABU87972 AAY08657 ABU84287 В Length 0000 Query 22131 220131 220085 2200860 2200860 2200860 2200860 2200860 220860 20080 20080 20080 Score Result

RESU AAB4 ID XX	RESULT 1 AAB48973 ID AAB48973 standard; protein; 3 XX	392 AA.
S,	AAB48973;	
1	27-MAR-2001 (first entry)	
(四)	Human Zsig13 variant #2, SEQ	SEQ ID NO:15.
₹ }	Human Zsiq13; serine protease	s; chromosome 11q22.1; elastase homologue;
Κ	glutamyl endopeptidase homolo	glutamyl endopeptidase homologue; factor X homologue; trypsin homologue;
3 3	trypsinogen homologue, mast c	trypsinogen homologue; mast cell protease homologue;
K.	alcohol production; laundry detergent component.	detergent component.
X 8	Homo sapiens.	
Z Z	US6153420-A.	
X &	28-NOV-2000.	
X &	04-MAY-1998; 98US-00072384.	
X 8	24-ADB-1997: 9711S-0044185D	
E E		
ž £	(ZYMO) ZYMOGENETICS INC.	
XZ	Sheppard PO;	
X:		
883	WPI; 2001-060090/07. N-PSDB; AAC91783.	
ž£	New isolated serine protease	(designated Zsig13), useful in industrial
F F	processes to degrade unwanted	processes to degrade unwanted proteins or alter the characteristics of
. E.	(e.g. brewing).	ייין מס אפון מס זון דווכנסנונטן מלאוונמנוכיים מווי מס אפון מס זון דווכנסנונטן מאאוונמנוכיים
X S S	Claim 1; Col 35-38; 26pp; English.	Jish.
ž	The invention relates to huma	The invention relates to human Zsiql3 proteins (AAB48972-B48974), and to
ខ្ល	DNA encoding them (AAC91782-C	د
႘	expression vectors and host c	expression vectors and host cells comprising a human Zsig13 DNA, and the
ပ္ပ	recombinant production of a h	numan Zaig13 protein or ita precursor. Zaig13
38	is a serine procease, and mas licheniformis glutamyl endope	is a serine procease, and has significant nomotogy to sacrifus licheniformis glutamyl endopeptidase, human clotting factor X, human
ပ္ပ	elastase, rat mast cell prote	mast cell protease, Streptomyces griseus trypsin, bovine

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 trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human
             Zsig13 is located on chromosome 11q22.1. Zsig13 is useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing compositions. It may also be used in industrial applications in which protease are utilised, including food processing, brewing and alcohol production, and as a component of a laundry detergent. The present sequence represents a human Zsig13 variant
                                                                                                                                                                                                                                1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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                                                                                                                                                                                                 Gaps
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                                                                                                                                                               Query Match 100.0%; Score 2131; DB 4; Length 392; Best Local Similarity 100.0%; Pred. No. 4.4e-151; Matches 392; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                  Sequence 392 AA;
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                                                                       New isolated serine protease (designated Zsigl3), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications
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                                                                                                                                                             Claim 1; Col 25-28; 26pp; English.
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Watches 385; Conservative
                 WPI; 2001-060090/07.
N-PSDB; AAC91782.
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RESULT 4

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This invention describes novel human transmembrane containing proteins and their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from nutritional uses, cytokine and cell differentiation, immune stimulation/suppression, haematopoiesis regulatory, tissue growth, activithibin, chemostatic/chemokinetic, haemostatic/thrombolytic, receptor/ligand, tumour inhibilory anti-inflammatory and other undefined activities. The cDNAs can be utilized as probes for gene diagnosis and as gene sources for gene therapy. The cDNAs can also be used for large scale expression of proteins. The transformed cells can be used for detection of the corresponding ligands and for screening of novel low-molecular
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inflammatories, immune stimulators/suppressors and tissue growth
regulatory tissue growth; inhibin; chemostatic; chemokinetic; haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory; gene therapy; screening.
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Matches 383; Conservative
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                                                                              Homo sapiens
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                                                                                                                                              Transmembrane domain; human; nutrition; cytokine; cell differentiation; immune etimulation; immune etimulation; immune etimulation; regulatory tissue growth; inhibin; chemostatic; chemokinetic; haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
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                                                                                                                 Human transmembrane domain containing protein from clone HP10493
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inflammatories, immune stimulators/suppressors and tissue growth
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100.0%; Pred. No. 2.8e-147;
ative 0; Mismatches 0;
                 AAY08657 standard; protein; 383 AA.
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KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
                                                                                                                                                                                                                                                                            Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scaring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                                      KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                            TYDLLYQQCDAQPGASGSGVYVRMKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                                       241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKOLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                                    Secreted protein; transmembrane protein; human; enterocolitis;
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                                                                                                                   361 ITPLKYAQICYWIKGNYLDCREG 383
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                                                                                                                                                                                      AAY13390 standard; protein; 383
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970S-0059184P
970S-0059268P
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970S-0062285P
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24-0CT-1997;
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21-0CT-1997;
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24-0CT-1997;
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ANY13344-403 represent secreted and transmembrane human proteins. The CDNA sequences are obtained from CDNA libraries, prepared from fetal Lung, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known concoded polypeptides e.g. PRO211 and PRO217 can be used for disorders associated polypeptides e.g. PRO211 and PRO217 can be used for disorders associated vith the preservation and maintenance of gastrointestinal mucosa and the crospal retrone, gastrointestinal ulceration and congenital microyllus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous and devolopment, diseases allowed of the vulva and gllomas), potent effects on cell growth and gllomas), potent effects on cell scort and development, diseases, Alzineimer's disease, Alzineimer's disease, Alzineimer's disease, Alzineimer's disease, Alzineimer's candevelopment of used as for fibromodulin, e.g. for reducing dermal scarring, PRO26 can be used as a target for anti-tumor drugs. PRO263 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may be used as an anti-thrombotic agent; PRO287 polypeptides and portions may be used for treating problems of the kidney, userus, endometrium, can be used for treating problems of the kidney, userus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated human genes and polypeptides used in, e.g. treatment of
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                                               97US - 0063738P
97US - 0064215P
97US - 0064210P
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97US - 0065186P
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Matches 383; Conservative
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              29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
31-OCT-1997;
31-OCT-1997;
03-NOV-1997;
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07-NOV-1997;
12-NOV-1997;
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This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The proteins which can be used for gene therapy and/or vaccination. The caids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 to collapse to collapse the produce TANGO 180 to TANGO 189 and TANGO 215 to collapse to detect and quantify the presence of TANGO nucleic acids in a sample and therefore identify or diagnose diseases associated to with inappropriate TANGO expression (e.g. diseases related to over or under expression of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a patients own production of the polypeptide of to rectify mutations that can may result in expression of an abnormally active polypeptide. The polypeptides may also be used to identify and produce agonists and antiadonists of TANGO expression and activity which may be used to modulate TANGO expression and diseases. The polypeptides are
                                                                                 241 IGMDYDYALLELKKPHKRKFWKIGVSPPAKQLPGGRIHPSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                                  360
301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                            241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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                                                                                                                                                                   301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine; secreted protein; transmembrane protein; gene therapy; vaccine;
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particularly useful for use as antigens for producing antibodies to TANGO proteins which may be used for inhibiting the activity of TANGO proteins. They may also be used to detect and quantify the presence of TANGO proteins in samples and therefore identify patients in whom the protein is over- or under-expressed. This sequence represents the human TANGO 186 protein described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimitation; cardiovascular; hepatotropic; antimitation; protropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasts; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
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                                                                                                                                                                                                                                                                                                                                                                  SGKSRRKRQIYGYDSRFSIFGKDFLLMYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
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                                                                                                                                                 Length 383;
                                                                                                                                                                                  0; Indels
                                                                                                                                                97.6%; Score 2080; DB 3; I
100.0%; Pred. No. 2.8e-147;
tive 0; Mismatches 0;
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98US-0094983P.
98US-0102686P.
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                                                                                                                                                                                Matches 383; Conservative
                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                    Sequence 383 AA;
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31-JUL-1998;
01-OCT-1998;
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human signal peptide-containing proteins HSPP-1 to HSPP-14. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of associated with decreased activity or function of HSPP. Antagonists of activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, creproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, alcrobial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's cirrhosis and monitoring, in gene therapy, as antisense, tripher-forming cor ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists or related diseases (in usual immunoassays), as therapeutic antagonists, including screens, and for purification of HSPP from natural
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                                                                                                                                                                                                                   New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
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                                                                            Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAGIPGLIFFLICAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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100.0%; Pred. No. 2...
0; Mismatches
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98US-0112129P
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                                     (INCY-) INCYTE PHARM INC
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Best Local Similarity
Matches 383; Conserv
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11-DEC-1998;
                                                                                                                     Bandman 0;
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AAYS3622-43 represent bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytckine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell innes, deficiencies. In addition, they may be used to support the growth and proliferation of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelosuppression, to support the growth and proliferation of megakaryocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve issue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions
                                                                                                                                                                                                                                                                                             Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoissis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; erythroid progenitor cell; colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; platelet disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone fracture; cartilage damage; artificial joint.
                                                                                                                                                                                                                                                          A bone marrow secreted protein designated BMS192
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361 ITPLKYAQICYWIKGNYLDCREG 383
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                                                                                                                            AAY53627 standard; protein; 383 AA
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30-SEP-1998;
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                                                                                                                                                                       AAY53627;
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and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints
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                                                                                                                                                                                                                                                                                                    SGKSRRKRQIYGYDSRFSIFGKDFLLAYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
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                                                                                                                                                                         1 MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                                                                                                                                                                              VSSSCGPQCHKGTPLPTYBEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
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                                                                                                          97.6%; Score 2080; DB 3; Length 383;
100.0%; Pred. No. 2.8e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                        Matches 383; Conservative
                                                                                                                           Similarity
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                                                                              Sequence 383 AA;
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Greene JM;
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Best Local 8
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The present interaction to a secreted protein sequences given in present interaction to the present interaction to the present interaction sequences given in AAA80660-A80623 encode the 12 secreted protein sequences given in AAA82660-A80623. The human secreted proteins have various activities of dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarteriosclerotic; antiarteriosclerotic seamples of which include: immune disorders e.g. antagonists and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatory disorders e.g. inflammatory bowel disease, cronnary atteriosclerosis and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma: The paraprotein and polymucleotide sequences and also as an an also and an application diseases. The human secreted protein gene cc and the treatment of infectious diseases. The human secreted protein gene #10 and protein gene #10 is located on chromosome 12.

Sequences AAB255616-825618 represent genes which are related to the coronary secreted protein gene#10
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                                       the prevention, amelioration and treatment of autoimmune, lammatory, hyperproliferative and cardiovascular disorders, cancer, ids, and infectious diseases.
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                                                                                                                                                                                                       secreted human
                                                                                                                                                                Disclosure, Page 169, 803pp, English.
                                                                                                                                                                                                       present invention relates to 12
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                   WPI; 2000-387742/33:
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inflammatory, }
wounds, and in:
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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS

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Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
                                                                                      antirheumātic, dermatologicāl; antiproliferative; antiarteriosclerotic; antidancer; vulnerary; antiviral; antibacterial; antidungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; corbn's disease, inflammatory disorder; inflammatory bowel disease; corbn's disease, nephritis; hyperproliferative disorder; cardiovascular disorder; cornary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human; chromosome 12.
                                                                            Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                 Protein encoded by human secreted protein gene #10 clone HUSQ05.
                                                                                                                                                                                                                                                                                                                                                  Kenny JJ,
                                                                                                                                                                                                                                                                                                                                                  Ruben SM, Olsen HS, Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 684-685; 803pp; English.
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                         (first entry)
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                         21-NOV-2000
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 AAB25592;
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Wei

Moore PA,

nucleotide sequences encoding them. The polynucleotide sequences given in present interiors and the sequences encoding them. The polynucleotide sequences given in AAB25576-B25593. The human secreted proteins activities of the proteins include: immunosuppressant; anti-inflammatory; antiarteriosclerotic; antiarcario, dermatological; antiproliferative; antiarteriosclerotic; antiarcarior, dispersed and proteins, polypeptides, agonists and antiqungal activity. The proteins, polypeptides, agonists and antiquose various disease, disperders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease,

Crohn's disease and nephritis; hyperproliferative disorders such as paraproteins and purpura, cardiovascular disorders e.g. coronary

The paraproteins and purpura; cardiovascular disorders e.g. coronary

arteriosclerosis and mycarditis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #10 and protein sequences are represented in sequences AA880615 and AA825585. Secreted protein gene #10 is located on chromosome 12. Sequences AAB25516-B2508 esquences and AAA80669-A80676 represent genes which are related to the sequences and AAA80669-A80676 represent genes which are related to the The present invention relates to 12 secreted human proteins and the

Sequence 383 AA;

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                                                                        1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                          Gaps
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                                       0; Indels
         Score 2080; DB 3; L
Pred. No. 2.8e-147;
97.6%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
         Query Match
Best Local Similarity 100.
Matches 383; Conservative
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Length 383;

Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens. 240 180 300 360 nootropic; neuroprotective; vasotropic; chemotaxic; angiogenic; anterthritic; antistentic; antistentic; antistentic; antistentic; antistentic; antistentic; antistentic; antistentic; antistentics; cardiant; antistentic; cerebroprotective; thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome; gastrointesfinal ulcexation; psoriasis; cancer; Parkinson's disease; Alzheimer's; ALS; neuropathy; dermal scarring; wound healing; nerve repair; thrombosis; bone; cartilage formation; angiogenesis; atheroacoloid arthritis; multiple sclarosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premature aging; AIDS; diabetes; stroke; gene therapy; transgenic; PRO; human. 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKOLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300 The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynucleotides of the invention may be useful as research tools and as therapeutics for treating enterocolitis, Zollingerantiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian; 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVARKHVLTAAHCIHDG 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND IGMDYDYALLELKKPHKRKFMKIGVSPPAKOLPGGRIHFSGYDNDRPGNLVYRFCDVKDE TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR Wood WI; Pennica D, Hillan K, Claim 12; SEQ ID NO 261; 355pp; English. 361 ITPLKYAQICYWIKGNYLDCREG 383 ITPLKYAQICYWIKGNYLDCREG 383 ADC78573 standard; protein; 383 Gurney AL, 99WO-US021090 98WO-US019330 01-JAN-2004 (first entry) (GETH) GENENTECH INC Human PRO307 protein. Goddard A, 2000-271434/23 N-PSDB; ADC78572 WO200015796-A2 Ното варіепв. 15-SEP-1999; 16-SEP-1998; 23-MAR-2000. ADC78573; 181 241 361 121 301 Chen J, Yuan J; RESULT 11 g ò a 8 셤 ò 셤 ò 셤 ò 셤

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WPI; 2001-081051/09
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Filvaroff E,
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08-SEP-1999;
13-SEP-1999;
15-SEP-1999;
05-OCT-1999;
30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
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        Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarring and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple sclerosis, inflammatory disorders, atheroseslerosis, cardiac injury, infertility, premature aging, AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
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                                                                                                                                                                                                                                             61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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                                                                                                                                                                                                                                                                                                                                                                                     241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                     1 MAGIPGLLFLLFFLLCAVGQVSPXSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLB
                                                                                                                                                                                                  1 MAGIPGLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                                                                                                                                                                                                                  VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
                                                                                                                                                                                                                                                                              SGKSRRKRQIYGYDSRPSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
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                                                                                                                                                               Gaps
 Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
                                                                                                                                                               ö
                                                                                                                                        Length 383;
                                                                                                                                       Match 97.6%; Score 2080; DB 3; Length 3 Local Similarity 100.0%; Pred. No. 2.8e-147; es 383; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ITPLKYAQICYWIKGNYLDCREG 383
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99US-0145698P.
99US-0146222P.
                                                                                            PRO protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schaemia; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO307 protein.
                                                                                                                   Sequence 383 AA;
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26-JUL-1999;
28-JUL-1999;
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                                                                                                                                        Query Match
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The present sequence is one of sixty one novel secreted and transmembrane diseases (e.g. pooriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enerocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischemias such as coronary ischemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), inflammatory infertility, AlDS and diabetes and retinal disorders with as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.6%; Score 2080; DB 4; L 100.0%; Pred. No. 2.8e-147; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 96; 393pp; English.
                                                                                                                                                               99WO-US028564.
99WO-US028565.
99WO-US030095.
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99WO-US030999.
2000WO-US000219.
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99WO-US028214.
99WO-US028313.
99WO-US020944
99WO-US021090
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Matches 383; Conservative
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301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                                                                                                                                                               Human Zsigl3; serine protease; chromosome 11q22.1; elastase homologue; glutemyl endopoptidase homologue; factor X homologue; trypsinogen homologue; mast cell protease homologue; collagenase homologue; protein degradation; food processing; brewing; alcohol production; laundry detergent component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated serine protease (designated Zsigl3), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.6%; Score 2080; DB 4; Length 383; 100.0%; Pred. No. 2.8e-147; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                Human Zsigl3 variant #3, SEQ ID NO:18
                                                                                                                                                          AAB48974 standard; protein; 383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Col 41-44; 26pp; English.
                                  361 ITPLKYAQICYWIKGNYLDCREG
                                                                 361 ITPLKYAQICYWIKGNYLDCREG
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98US-00062142.
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N-PSDB; AAC91784.
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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17-APR-1998;
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                                                                                                                                                    241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                                                      TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                  61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVG1Y1LSSSGDGAQHRDSGS
                                                                                                                 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
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                                                  SCKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
                                                                                                    KTYVKGTOKLRVGFLKPKFKDGGRGANDSTSAMPEOMKFOWIRVKRTHVPKGWIKGNAND
                                                                                                                                                                    241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDB
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                                                                                                                                                                                                                                                                       AAU29048 standard; protein; 383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO polypeptide sequence #25.
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2000US-0198585P.
2000US-0199397P.
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14-MAR-2000;
15-MAR-2000;
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21-MAR-2000;
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29-MAR-2000;
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04-APR-2000;
04-APR-2000;
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18-APR-2000;
25-APR-2000;
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1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGABAKLE

Matches 383; Conservative

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Human, PRO, cytostatic; tumour; cancer; breast; lung; stomach; liver;
dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
                                                                                ABU58424 standard; protein; 383 AA
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9705-0063120P

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98US-0083495P.
98US-0083495P.
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                                                                                                                                                                                                                                                                                                                                                                            15-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO polypeptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS2003027272-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
31-0CT-1997;
31-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1997;
18-DEC-1997;
10-MAR-1998;
11-MAR-1998;
20-MAR-1998;
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12-DEC-1997;
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24-OCT-1997
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The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNP) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
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Smith V, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Fig 50; 774pp; English.
                                                                             2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
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2000WO-US030952.
2000WO-US032678.
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2000WO-US020710.
2000US-00644848.
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N-PSDB; AAS45949.
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22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
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28-JUL-2000;
22-AUG-2000;
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PR 05-APR-1998 98US -0083456 P.
PR 07-APR-1998 98US -0083456 P.
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PR 02-JUN 1998 98US -00832 P.
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PR 11-JUN 1998 98US -00832 P.
PR 24-JUN 1998 98US -00833 P.
PR 24-JUN 1998 9
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PR 02-ULL-1998 99US-001652P.
PR 24-ULL-1998 99US-001652P.
PR 10-AUG-1998 99US-001652P.
PR 10-AUG-1998 99US-001652P.
PR 11-AUG-1998 99US-001652P.
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PR 26-AUG-1998 99US-001665P.
PR 26-AUG-1998 99US-001752P.
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PR 10-SEP-1998 99US-010166P.
PR 11-SEP-1998 99US-010166P.
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PR 21-SEP-1998 99US-010166P.
PR 21-SEP-1998 99US-010173P.
PR 21-SEP-1998

Query Match 97.6%; Score 2080; DB 6; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.8e-147;
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps

MAGIPGLLFLIFFLLCAVGOVSPXSAPWKPTWPAYRLPVVLPOSTLNLAKPDFCAEAKLE

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        Db
        61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120

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        Cy
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Search completed: July 1, 2005, 21:03:28 Job time : 102.435 secs THIS PAGE BLANK (USPTO)

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NAME/KEY: Signal Sequence LOGATION: 1...19
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14, Appl
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12, Appl
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8, Appli
13989, A
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Sequence 2, Appli
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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-09-902-540-12881
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US-09-905-125A-261
US-09-902-775A-261
US-09-906-700-261
US-09-903-603A-261
US-09-904-920A-261
US-09-909-064-261
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5-09-551-826D-12
5-09-949-016-8220
5-09-551-826D-8
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-09-906-618-261
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-09-551-826D-14
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-09-551-826D-10
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-09-551-826D-2
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No.	5223425-8	9	253	5.3	114	44
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Seguence 44, Appl	US-08-944-483-44	ო	228	5.3	114	42
59	US-08-944-483-59	ო	241	5.4	115.5	41
Sequence 2, Appli	US-08-487-037-2	н	437	5.5	117	40
7,	US-10-042-091A-7	4	284	5.6	120	33
7,	US-10-041-400A-7	4	284	5.6	120	38
Sequence 7, Appli	US-09-387-375-7	4	284	9.	120	37
89,	PCT-US95-14442A-89	Ŋ	256	5.7	122	36
Sequence 89, Appl	US-08-906-613-89	٣	256	5.7	122	32
	US-09-012-692-89	m	256	5.7	122	34
32,	US-09-032-215-32	m	256	5.7	122	33
89,	æ	ო	256	5.7	122	32
89,	US-08-639-075A-89	ო	256	5.7	122	31
Seguence 89, Appl	US-08-817-795-89	m	256	5.7	122	30
Seguence 89, Appl	US-08-906-616-89	ო	256	5.7	122	29
Sequence 89, Appl	US-08-906-769-89	m	256	5.7	122	28

ALIGNMENTS

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Best Local Similarity 98.2
Matches 385; Conservative
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APPLICATION NUMBER: US
FILING DATE:
                    TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
      STRANDEDNESS: single
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                                                                                                    1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
  Length 392;
                                        Indels
Ouery Match 100.0%; Score 2131; DB 3; Best Local Similarity 100.0%; Pred. No. 1.5e-225; Matches 392; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ITPLKYAQICYWIKGNYLDCREGDTVFPPGSN 392
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STUTARE: FREAKSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
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...ERIALS A.
...DRESS:
...KET: 1201 Eastlake Avenue East CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER PT
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Patent No. 6153420
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REPERBUCK/DOCKET NUMBER: 97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 392 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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NAME: Parker, Gary E
REGISTRATION NUMBER: 31,
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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US-09-072-384-2
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Sequence 18, Application US/09072384

Sequence 18, Application US/09072384

Patent No. 615342

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: SRINE PROTEASE POLYPEPTIDES

TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
                                                                                                                                    97.8%; Score 2085; DB 3; Length 392; 98.2%; Pred. No. 1.8e-220; Live 1; Mismatches 6; Indels
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COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DOSS
SOFTWARE: FRASTEM: DOS
SOFTWARE: FRASTEM FOR Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
NAME/KEY: Signal Sequence LOCATION: 1...19
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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120
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100.0%; Pred. No. 6e-220;
tive 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                      CURRENT PILLING DATE: 10466-14

CURRENT PILLING DATE: 2001-07-17

PRICA PAPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/2054

PRIOR APPLICATION NUMBER: PCT/US99/2054

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR PILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR PILING DATE: 1999-11-05

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-05

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-05

PRIO
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Secreted and Transmembrai
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                   Williams, P. Mickey
Wood, William, I.
                                                                                                                                                Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                      Paoni, Nicholas F
                                   Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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; ORGANISM: Homo Sapien
US-09-907-794A-261
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Best Local 9
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                                                                                           APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.6%; Score 2080; DB 3;
100.0%; Pred. No. 6e-220;
iive 0; Mismatches 0;
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REBERGENCE/POCKET NUMBER: 97-16C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 261, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Botetein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Bllen
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Signal Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 1...19
; OTHER INFORMATION:
US-09-072-384-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-907-794A-261
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us-09-658-677-15.rai

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Query Match 97.6%; Score 2080; DB 4; Best Local Similarity 100.0%; Pred. No. 6e-220; Matches 383; Conservative 0; Mismatches 0;
| PRIOR APPLICATION NUMBER: PCT/US99/28564 |
| PRIOR FILING DATE: 1999-12-02 |
| PRIOR FILING DATE: 1999-12-02 |
| PRIOR PELING DATE: 1999-12-02 |
| PRIOR FILING DATE: 1999-12-16 |
| PRIOR FILING DATE: 1999-12-16 |
| PRIOR FILING DATE: 1999-12-16 |
| PRIOR FILING DATE: 1999-12-20 |
| PRIOR FILING DATE: 1999-12-20 |
| PRIOR PILING DATE: 2000-01-05 |
| PRIOR PILING DATE: 2000-01-05 |
| PRIOR PILING DATE: 2000-01-05 |
| SEQ ID NO 261 |
| LENGTH: 383 |
| TYPE: PRI |
| ORGANISM: Homo Sapien |
| US-09-905-125A-261 |
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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; Sequence 261, Application US/09902775A
; Patent No. 6686451
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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GENERAL INFORMATION:
APPLICANT: Genenech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desnoyers, Luc
Eaton, Dan L.
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Tunas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: William, I.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION WIMBER: US (0) 4414
PRIOR FILING DATE: 1999-00-26
PRIOR PLING DATE: 1999-00-13
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-00-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-00-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-00-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-10-05
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/23089
241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                         IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                         US-09-905-125A-261

Sequence 261, Application US/09905125A
Parent No. 6664376
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bankenazi, Avi
APPLICANT: Betsein, David
APPLICANT: Betsein, David
APPLICANT: Betson, Dan L.
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Grimaldi, Christopher J.
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Hillan, Kenneth, J
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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                                                                                                                                                                    TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,700

CURRENT APPLICATION NUMBER: US/09/906,700

CURRENT FILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PLING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR PILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28313
                                                                                                                                                                                                                                                                                    361 ITPLKYAQICYWIKGNYLDCREG 383
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; Sequence 261, Application US/09906700
; Patent No. 6723535
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Stewart, Timothy A.
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Eaton, Dan L.
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Sao, Wei-Qiang
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Stewart, ....
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APPLICANT: Genented
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                                                                                                                                                                                                                                                      and Transmembrane Polypeptides and Nucleic
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Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT PILING DATE: 2001-07-10
PRIOR PAPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-13
                                                                                                                                                                                              PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembran
ITLE OF INVENTION: Acids Encoding the Same
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PRIOR PELING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
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PRIOR FILING DATE: 2000-01-05
SEQ ID NO 261
LENGTH: 383
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PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/21547
                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                        Paoni, Nicholas F.
  Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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; ORGANISM: Homo Sapien
US-09-902-775A-261
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APPLICANT: ROY, MARIOLAGE F.
APPLICANT: ROY, MARIOLAGE F.
APPLICANT: SOY, MARIOLAGE F.
APPLICANT: SOY, MARKEY
APPLICANT: SEWARTE, Timothy A.
APPLICANT: Mood, Williams, P. Mitkey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
CURRENT PILIANT DATE: US/09/093, 603A
CURRENT FILING DATE: 1030-07-11
FRIOR PELING DATE: 2001-07-11
FRIOR PELING DATE: 1030-07-07-11
FRIOR APPLICATION NUMBER: PCT/US99/2034
FRIOR APPLICATION NUMBER: PCT/US99/2034
FRIOR APPLICATION NUMBER: PCT/US99/2034
FRIOR APPLICATION NUMBER: PCT/US99/2031
FRIOR PELING DATE: 1939-11-20
FRIOR FILING DATE: 1939
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100.0%; Pred. No. 6e-220;
ive 0; Mismatches 0;
                                                             Paoni, Nicholas F.
Roy, Margaret Ann
             Mather, Jennie P.
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Best Local Similarity 100.
Matches 383; Conservative
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; ORGANISM: Homo Sapien
US-09-903-603A-261
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97.6%; Score 2080; DB 4,
Best Local Similarity 100.0%; Pred. No. 6e-220,
Matches 383; Conservative 0; Mismatches (
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR RPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 383
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Botsein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong. Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-700-261
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100.0%; Pred. No. 6e-220;
tive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/US99/28565.
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
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Patent No. 6818449
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Oiang
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Hillan, Kenneth, J
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Gerritsen, Mary E
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Best Local Similarity 100.0
Matches 383; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Mather, Jennie
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo Sapien
US-09-904-920A-261
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APPLICANT:
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Grimaldi, Chr.
Gurnery, Austin, L.
Hillan, Kenneth, J.
Hillan, Kenter, Johnse F.
ANT: Nunse, Daniel
ANT: The Rouni, Nicholas F.
ANT: Williams, Paniel
ANT: Williams, Paniel
ANT: Williams, Paniel
ANT: Williams, P. Mickey
ANT: Wood, William, P. Mickey
C. INVENTION: Acids Encoding the Same
ARMT FILMS ONTS: 2010-07-13
IGR APPLICATION NUMBER: US/09/904,920A
RIGHT FILMS ONTS: 2010-07-13
IGR APPLICATION NUMBER: US/01/014
ARIOR FILMS ONTS: 1999-07-26
RIGH FILMS ONTS: 1999-07-36
RIGH FILMS ONTS: 1999-07-37
ATE: 1999-11-30
TCATION NUMBER: PCT/US99/2854
                                                       301 TYDLLYQQCDAQPGASGSGVYVRWWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                          IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                 301 TYDLLYQQCDAQPGASGSGVYVRWWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                                                                                                        361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                             361 ITPLKYAQICYWIKGNYLDCREG 383
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Patent No. 6806352
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara, Napoleone
Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Eaton, Dan L.
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us-09-658-677-15.rai

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361 ITPLKYAQICYWIKGNYLDCREG 383
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Patent No. 6818746
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Hillan, Kenneth, J.
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Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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                                                                                                                                                                                TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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Best Local Similarity 100.0%; Pred. No. 6e-220;
Matches 383; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                       CURRENA FILLING DATE: 2001-07-18

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1099-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR PLING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-18

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-06

PRIOR PILING DATE: 1999-12-07

PRIOR PILING DATE: 1999-12-07
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/909,064 CURRENT FILING DATE: 2001-07-18
                                                                       Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo Sapien
US-09-909-064-261
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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                                                                                                  APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                    TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
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CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT PILING DATE: 2001-07-13

PRIOR PELICATION NUMBER: US/09/905,381A

PRIOR PELICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1099-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PELING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-11-20
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APPLICANT: Tunans, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Worliams, P. Mickey
APPLICANT: Worliams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
CURRENT FILMS 10466-44
FILE REPERBACE 10466-44
FILE REPERBACE 10466-44
FRICK APPLICATION NUMBER: US/09/906,618
CURRENT APPLICATION NUMBER: DATA 048
FRICK APPLICATION NUMBER: US 60/143,048
FRICK APPLICATION NUMBER: US 60/145,698
FRICK APPLICATION NUMBER: US 60/146,698
FRICK APPLICATION NUMBER: US 60/146,222
FRICK APPLICATION NUMBER: US 60/146,222
FRICK APPLICATION NUMBER: PCT/US99/20594
FRICK FILING DATE: 1999-07-26
FRICK FILING DATE: 1999-07-28
FRICK FILING DATE: 1999-07-38
FRICK FILING DATE: 1999-01-38
FRICK FILING DATE: 1999-01-38
FRICK FILING DATE: 1999-11-30
FRICK FILING DATE: 1999-11-30
FRICK FILING DATE: 1999-11-30
FRICK FILING DATE: 1999-11-20
FRICK APPLICATION NUMBER: PCT/US99/28313
FRICK FILING DATE: 1999-11-20
FRICK APPLICATION NUMBER: PCT/US99/28014
FRICK APPLICATION NUMBER: PCT/US99/28016
FRICK APPLICATION NUMBER: PCT/US99/28016
FRICK APPLICATION NUMBER: PCT/US99/30091
FRICK FILING DATE: 1999-11-20
FRICK FILING DATE: 1999-11-20
FRICK FILING DATE: 1999-12-20
FRICK FILING DATE
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100.0%; Pred. No. 6e-220;
tive 0; Mismatches 0
                                   Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Best Local Similarity 100.
Matches 383; Conservative
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US-09-906-618-261
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 383
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Patent No. 6828146
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
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Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Mather, Jennie P
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Matches 383; Conservative
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ORGANISM: Homo Sapien
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301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                         85 LSYETLYANGSRIETQV----GIYILSSSGDG-----AQHRDSGSSGKSRRKRQIYG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 YDSRFSIFGKDFLLNYPFSTSVKLST---GCTGTLVAEKHVLTAAHCIHD-GKTYVKGTQ 188
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APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Lansidensen, Claus Bo Voge
APPLICANT: Lansidensen, Soren Flensted
TITLE OF INVENTION: No. 655893991 Proteases And Variants Thereof
FILE REPERENCE: 5665.200-US
CURRENT APPLICATION WHORER: 2000-04-17
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APPLICANT: Christensen, Claus Bo Voge
APPLICANT: Lassen, Soren Flensted
TITLE OF INVENTION: No. 6558939el Ptoteases And Variants Thereof
FILE REFERENCE: 5665.200-US
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9.5%; Score 202.5; DB 4; Length 314;
Best Local Similarity 24.8%; Pred. No. 2.1e-13;
Matches 77; Conservative 37; Mismatches 137; Indels 59
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APPLICANT: No. 655893 regaard-Madsen, Mads
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                                                                                                                                              361 ITPLKYAQICYWIKGNYLDCREG 383
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Patent No. 6558939
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SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                           Length 316;
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9.1%; Score 193; DB 4; L.
Best Local Similarity 24.0%; Pred. No. 2.3e-12;
Matches 79; Conservative 43; Mismatches 143;
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CURRENT APPLICATION DATA:
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APPLICANT: Budtz, Peter
APPLICANT: Nielsen, Per M.
TITLE OF INVENTION: PROTEIN PREPARATIONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CURRENT APPLICATION NUMBER: US/09/551,826D
CURRENT FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VEXSION 3.2
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PILING DATE: 06-FBB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00036
FILING DATE: 06-FBB-1992
ATTORNEY/AGENT INFORMATION:
NAME: AGTIS, Cheryl H.
REGISTRATION NUMBER: 34,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: United States of America ZIP: 10174-6201
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/090,048
FILING DATE: 16-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-090-048-1; Sequence 1, Application US/08090048; Patent No. 5523237
                                                                                                                                                                  TYPE: PRT ORGANISM: Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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CITY: New York
                                                                                                                                                                                                                           US-09-551-826D-2
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                                                                                                               SEQ ID NO 2
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148 YPFSTSVKLST---GCTGTLVAEKHVLTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 RGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 GVSPPAKOLPGGRIHFSGYDNDRPGNLVYRFCD--VKDETYDLLYQQCDAQPGASGSGVY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.3%; Score 177; DB 1; Length 222;
Best Local Similarity 25.5%; Pred. No. 7.6e-11;
Matches 60; Conservative 27; Mismatches 104; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 VRMWKRQQQKWERKII----GIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | : | : | : | 113 EQSSSRINCSGPCSLAVHTNGVYGG-----SSYNRGTRITKEVFDNLTNW 217
REFERENCE/DOCKET NUMBER: 3396.214-US
TELECOMMUICATION:
TELEPHONE: 212-867-0123
TELEPAX: 212-867-0298
                                                               TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDENDESS: single
STRANDENDESS: single
MOLECULE TYPE: protein
US-08-090-048-1
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Search completed: July 1, 2005, 21:10:43 Job time: 27.5364 secs

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July 1, 2005, 21:08:25; Search time 90.3582 Seconds (without alignments) 1673.692 Million cell updates/sec
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1 MAGIPGLLFLLFFLLCAVGQ.....IKGNYLDCREGDTVFPPGSN 392
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1: \cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
3: \cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: \cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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19: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
10: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
17: \cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
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	Description	Sequence 12, Appl	Sequence 261, App	261,	Sequence 261, App	261,	261,	261,	261	Sequence 261, App	261	Sequence 261, App
SUMMARIES	ID	US-09-765-205-12	US-09-909-320-261	US-09-909-088B-261	US-09-905-291A-261	US-09-902-853-261	US-09-907-824-261	US-09-907-841-261	US-09-904-011-261	US-09-903-640-261	US-09-908-093-261	US-09-906-742-261
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	* Query Match Length DB	383	383	383	383	383	383	383	383	383	383	383
	Query Match	97.6	97.6	97.6	97.6	97.6	97.6	97.6	97.6	97.6	97.6	97.6
	Score	2080	2080	2080	2080	2080	2080	2080	2080	2080	2080	2080
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App	App
2261, 2261,	
Sequence Seq	Sednence
US-09-906-838-261 US-09-907-613-261 US-09-904-859-261 US-09-904-859-261 US-09-904-86-261 US-09-904-786-261 US-09-904-786-261 US-09-906-700-261 US-09-906-700-261 US-09-903-786-261 US-09-903-786-261 US-09-903-786-261 US-09-903-786-261 US-09-903-786-261 US-09-903-786-261 US-09-903-786-261 US-09-903-786-261 US-09-903-913-261 US-09-903-925-261 US-09-903-520-261 US-09-903-520-261 US-09-903-520-261 US-09-903-520-261 US-09-903-520-261 US-09-903-520-261 US-09-904-482-261 US-09-904-88-261 US-09-904-88-261 US-09-904-88-261 US-09-905-88-261 US-09-905-88-261 US-09-905-88-261 US-09-905-88-261 US-09-905-88-261 US-09-905-88-261	-09-902-759-2 -09-902-634-2
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111 112 113 114 115 115 115 115 115 115 115 115 115	

ALIGNMENTS

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAGIPGLIFILFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                APPLICANT: Cao, Li
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001.01-17
PRIOR APPLICATION NUMBER: US/09/212,440
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               97.6%; Score 2080; DB 9; I
100.0%; Pred. No. 2.2e-193;
tive 0; Mismatches 0;
                    Sequence 12, Application US/09765205
Patent No. US20020034800A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: human
US-09-765-205-12
US-09-765-205-12
                                                                                                                                                                                                                                                                                                            LENGTH: 383
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-261
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
PRIOR PILLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILLING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-07-26
PRIOR PILLING DATE: 1999-07-28
PRIOR PILLING DATE: 1999-09-08
PRIOR PILLING DATE: 1999-09-08
PRIOR PILLING DATE: 1999-09-13
PRIOR PILLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: CTT/US99/21090
PRIOR PILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: CTT/US99/21090
PRIOR PILLING DATE: 1999-09-15
PRIOR PILLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: CTT/US99/21090
                                                                                                                                   300
                                                                     181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
                                                                                                                                                          241 IGMDYDYALLELKKPHKRKFWKIGVSPPAKQLPGGRIHPSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                                                                                                  301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
                                                                                                                                   241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
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FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                                                                                                                              361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                                                                                                                          Sequence 261, Application US/09909320
Patent No. US2002013240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eston, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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100.0%; Pred. No. 2.2e-193;
tive 0; Mismatches 0;
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION WUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-03
PRIOR PLILING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR PRILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NOS: 423
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Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botherazi, Avi
APPLICANT: Betrein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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Goddard, A.
Godowski, Paul J.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Best Local Similarity 100.
Matches 383; Conservative
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT APPLICATION NUMBER: PCT/US00/0414
PRIOR PILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-013
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21847
PRIOR PILING DATE: 1999-10-15
                                                                                                                                                                                                                                                                                                                         301 TYDLLYQQCDAQPGASGSGYVVRWWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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                                                                  181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQMIRVKRTHVPKGWIKGNAND
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Patent No. US20020160374A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
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PRIOR PELING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-09
PRIOR PELING DATE: 1999-09-09
PRIOR PELING DATE: 1999-09-09
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-10-05
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PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-06
PRIOR PELING DATE: 1999-12-20
Grimaldi, Christopher J.
                                                                                                                        Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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                                                                                             Kljavin, Ivar J
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; LENGTH: 383
; TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-261
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/665,350
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-13-09
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PRIOR FILING DATE: 1999-13-09
PRIOR FILING D
     Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Williams, P. Mickey
Wood, William, I.
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Stewart, Timothy A.
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Paoni, Nicholas F.
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Best Local Similarity 100.
Matches 383; Conservative
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US-09-902-853-261
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                                           PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30091
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-05
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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Botstein, David
Botstein, David
Benoyers, Luc
Baton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Clang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Paul J.
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Publication No. US20020192659A1
GENERAL INFORMATION:
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APPLICANT: Ashkenzi, Avi
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napolec
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; ORGANISM: Homo Sapien
US-09-905-291A-261
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    Length 383;
                                            Indels
97.6%; Score 2080; DB 9; I
100.0%; Pred. No. 2.2e-193;
ive 0; Mismatches 0;
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181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
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Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PLENGTH: 383
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Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Filvaroff, Ellen
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Goddard, A.
Godowski, Paul J.
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Gao, Wei-Qiang
Gerber, Hanspeter
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-09-907-841-261
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APPLICANT:
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APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Scewart. Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Acids Encoding the Same
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-38
PRIOR PILING DATE: 1999-07-38
                                                                                                                                                                                                                    TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
        KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
                                                                                                                                                               241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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                                    KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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Sequence 261, Application US/09907824
Publication No. US20020197671A1
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Grimaldi, Christopher J.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Hillan, Kenneth, J
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
Pan, James
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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SEQ ID NO 261
LENGTH: 383
TYPE: PRT
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APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane JITLE OF INVENTION: Secreted and Transmembrane JITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 Encoding the Same CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2000-02-2
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-15
Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F. Roy, Margaret Ann
                                                                                                                                                                                                                                                                                Stewart, Timothy A. Tumas, Daniel
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Best Local Similarity 100.0
Matches 383; Conservative
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and Transmembrane Polypeptides and Nucleic
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361 ITPLKYAQICYWIKGNYLDCREG 383
                                        Sequence 261, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, A.
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Mather, Jennie P.
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Eaton, Dan L.
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Gao, Wei-Qiang
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 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURENT APPLICATION NUMBER: US/09/903,640
PRIOR PAPLICATION NUMBER: 09/665,350
PRIOR PLICATION DATE: 2001-07-11
PRIOR PLICATION DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
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Pred. No. 2.2e-193;
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V 100.0%; Pred. No. ...
O; Mismatches
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Publication No. US20030017498A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Paoni, Nicholas F
Roy, Margaret Ann
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Best Local Similarity
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97.6%; Score 2080; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USO0/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
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Grimaldi, Christopher J.
Gurney, Auerin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
Fong, Sherman
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Goddard, A.
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Paoni, Nicholas F.
Roy, Margaret Ann
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Gerber, Hanspeter
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APPLICANT: Ashkenai, Avi
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                               ORGANISM: Homo Sapien
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Publication No. US20030023054A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Gao, Wei-Qiang
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                                                                                                                                                                                          CURRENT PELLICATION NUMBER: US/09/908,093
CURRENT PELLING DATE: 2001-07-17
PRIOR PEPLICATION NUMBER: US/665,350
PRIOR FILING DATE: 2000-02-2
PRIOR FILING DATE: 2000-02-2
PRIOR PELLING DATE: 1090-07-07
PRIOR PELLING DATE: 1090-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PELLON NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-15
PRIOR PELLON NUMBER: PCT/US99/23109
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: PCT/US99/30099
PRIOR FILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12
   Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Best Local Similarity 100.0
Matches 383; Conservative
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ORGANISM: Homo Sapien
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: 10466-14
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
FRIOR PILING DATE: 2000-09-18
FRIOR PILING DATE: 2000-09-18
FRIOR PLILING DATE: 2000-02-22
FRIOR PILING DATE: 2000-02-22
FRIOR PILING DATE: 1999-07-07
FRIOR PILING DATE: 1999-07-07
FRIOR PILING DATE: 1999-07-26
FRIOR PILING DATE: 1999-07-26
FRIOR PILING DATE: 1999-07-26
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-07-28
FRIOR PILING DATE: 1999-09-13
FRIOR PILING DATE: 1999-09-13
FRIOR PILING DATE: 1999-09-15
FRIOR PILING DATE: 1999-10-05
FRIOR PILING DATE: 1999-10-05
FRIOR PILING DATE: 1999-11-29
FRIOR PILING DATE: 1999-11-20
TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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                                                                                                                                                                                                             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITILE OF INVENTION: Acids Encoding the Same
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100.0%; Pred. No. 2.2e-193;
ive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/906,838

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: US/09/906,838

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR PRILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-11-30

PRIOR FILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

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PRIOR PILIN
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Best Local Similarity 100.
Matches 383; Conservative
                                                                                                                    Tumas, Daniel
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; ORGANISM: Homo Sapien
US-09-906-838-261
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97.6%; Score 2080; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 383; Conservative 0; Mismatches 0;
                                            PRIOR PELICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
| LENGTH: 383
APPLICATION NUMBER: PCT/US99/28565
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Publication No. US20030027143A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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ilvaroff, Ellen
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Gerritsen, Mary B
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dur L.
APPLICANT: Eaton, Dan L.
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CORGANISM: Homo Sapien
US-09-906-742-261
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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.6%; Score 2080; DB 10;
100.0%; Pred. No. 2.2e-193;
tive 0; Mismatches 0;
PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION WUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR APPLICATION NUMBER: PCT/US99/30910

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

LENGTH: 383
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Publication No. US20030027146A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Bestein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Filvacoff, Ellen
APPLICANT: Filvacoff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Manspeter
APPLICANT: Gedard, A.
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Best Local Similarity 100.0
Matches 383; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-09-907-613-261
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APPLICANT:
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PLI
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         181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
                                                                                                   241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
                                                                                                                                                                                    301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                  241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                                                                   361 ITPLKYAQICYWIKGNYLDCREG 383
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Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-907-613-261
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APPLICANT:
MOGOL, MILIAGH.
MAPLICANT:
MOGOL, MILIAGH.
TITLE OF INVENTION: Secrete
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,859
CURRENT FILING DATE: 2001-07-12
FRIOR PLING DATE: 2000-09-18
FRIOR APPLICATION NUMBER: US 60/143,048
FRIOR PLING DATE: 2000-09-18
FRIOR PLING DATE: 1999-07-07
FRIOR PLING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-07
FRIOR PLING DATE: 1999-07-26
FRIOR PLING DATE: 1999-07-26
FRIOR PLING DATE: 1999-07-26
FRIOR PLING DATE: 1999-07-26
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR APPLICATION NUMBER: PCT/US99/2094
FRIOR PLING DATE: 1999-09-08
FRIOR FILING DATE: 1999-09-08
FRIOR FILING DATE: 1999-09-15
FRIOR PLING DATE: 1999-09-15
FRIOR PLING DATE: 1999-09-15
FRIOR PLING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-10-05
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-29
FRIOR FILING DATE: 1999-11-30
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                                IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                              241 IGMDYDYALLELKKPHKRKFWKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
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Publication No. US20030036060A1
GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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US-09-904-859-261
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APPLICANT:
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                                                                                                                                                                              APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                          TILLE CPT INVENTION: ACIDS ELECOLLING THE EVERBRUCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,942

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: PT/US00/04114

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-12-0

PRIOR PLING DATE: 1999-12-0

PRIOR PLING DATE: 1999-12-0

PRIOR FILING DATE: 1999-12-0

PRIOR FILING DATE: 1999-12-0

PRIOR PRILING DATE: 1999-12-0

PRIOR FILING DATE: 1999-12-0

PRIOR PRILING DATE: 1999-12-0
                                                                                        Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                           soni, Nicholas F
Mather, Jennie P.
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.6%; Score 2080; DB 10; Length 383; Best Local Similarity 100.0%; Pred. No. 2.2e-193; Matches 383; Conservative 0; Mismatches 0; Indels 0
                           PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION WUMBER: PCT/US99/28565
PRIOR APPLICATION WUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FLING DATE: 1999-12-16
PRIOR PLILING DATE: 1999-12-20
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PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 2000-01-05
PRIOR FILING DATE: 2000-01-05
APPLICATION NUMBER: PCT/US99/28564
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Job time : 91.3582 secs
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GenCore version 5.1.6	31
Copyright (c) 1993 - 2005 Compugen Ltd.	32
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OM protein - protein search, using sw model	35
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Run on: July 1, 2005, 20:54:23 ; Search time 20.826 Seconds	37
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1811.048 Million cell updates/sec	36
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US-09-658-677-15 2131 1 MAGIPGLLFLLCAVGQ.....IKGNYLDCREGDTVFPPGSN 392 283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	endopeptidase (EC	metalloproteinase	choline binding pr	coaqulation factor	pancreatic elastas	hypothetical prote	pancreatic elastas	pancreatic elastas	pancreatic elastas	probable pancreati	trypsin-like prote	choline binding pr	complement factor	pancreatic elastas	pancreatic elastas	trypsin (EC 3.4.21	hypothetical prote	Putative protease	coagulation factor	brain-specific ser	pancreatic elastas	coagulation factor	hypothetical prote	probable secreted	probable pepetidas	complement factor	serine proteinease	masquerade precurs	T-cell suppressor
SUMMARIES	A45134	A35122	E97915	EXRT	A26823	T29767	B26823	A25528	S70439	A56615	TRWVSY	C95045	DBHU	ELPG	ELRT1	TRSMG	E85765	H64915	EXHU	JC5759	C26823	EXBO	T15308	T35117	AH0282	A29154	A47547	A55617	A28566
% Query Match Length DB	316	313 2	218 2	482 1	269 2	522 2	269 2	271 2	258 4	267 4	238 1	285 2	246 1	266 1	266 1	259 1	273 2	273 2	488 1	761 2	269 2	492	1582 2	405 2	278 2	583 2	786 1	1047 2	236 2
% Query Match L	 Α.	6.4	6.1	5.7	9.6	5.5	5.4	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.2	5.2	5.2	5.5	5.5	5.1	5.1	5.1	5.1	5.1	5.0
Score	4.4	135.5	131	120.5	119	117	115.5	115.5	115	115	114.5	114.5	114	113	113	112.5	112.5	112.5	111.5	111	110	110	110	109.5	109	108	108	108	107.5
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Ra-reactive factor trypsin-related pr	pancreatic elastas	coagulation factor	hypothetical prote	trypsin-like prote	membrane-bound arg	trypsin (EC 3.4.21	probable trypsin V	probable polygalac	probable secreted	coagulation factor	complement factor	coagulation factor	allergen Der f III	factor IX - rabbit
A59271 S40004	ELRT2	KFBO	T34929	JC4170	JC7731	S40006	D82175	T02289	T35118	A30351	151579	A38738	S68424	146712
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ALIGNMENTS

A45134 endopeptidase (EC 3.4 C;Specias: Bacillus lich C;Date: 10-Unn-1993 #seg C;Accession: A45134; S23 R;Kakudo, S.; Kikuchi, N J. Biol. Chem. 267, 2378 A;Title: Purification, c A;Reference number: A451 A;Reference number: A451 A;Retersion: A45134 A;Retersion: Purification, c A;Rocession: A45134 A;Reterence number: A451 A;Reterence sequence extract B;Svendsen, I:; Breddam, Eur. J. Biochem. 204, 16 A;Reference number: S23 A;Reference number: S33 C;Superfamily: Glutamyl C;Superfamily: Glutamyl C;Reywords: hydrolase	-),, eeni, 2-2, 2-2, 2-3, 34; 78; 78; 78;
Outery Meat Condens Matches 79 QY 63 QY 120 QY 120 QY 171 Db 177 QY 230 Db 179 Db 179	Watch Macch 10 State 194; Score 194; De 2; Dength 318; Matches 79; Conservative 43; Mismatches 143; Indels 64; Gaps 15; 63 SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRIETCVGIYILSSGGDGAQHRDSG 119; 10 SSGKSRRKRQIYGYDSRFSIFGKDFLNNIKSDOYGLYSKAFTGTGKVNETKE 79 120 SSGKSRRKRQIYGYDSRFSIFGKDFLNYPFSTSVKLSTGCTGTLVAEKHV 170; 1

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A;Cross-references: UNIPROT:QBDR41; GB:AE007317; PIDN:AAK99153.1; PID:g15457907; GSPDB:GP
C;Genetics:
A;Gene: cbpG-truncation
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A;Residues: 1-482 <STA1>
A;Cross-references: UNIFROT:Q63207; EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g5066(
A;Note: submitted to the EMBL Data Library, June 1994
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
V. R.; Blanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.;
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MuID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       choline binding protein G, truncation [imported] - Streptococcus pneumoniae (strain R6)
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176 -SGTMFYSVK-GWTESKDTNYDYGAIKLNGSPGNTVGW-YGYRTTNSSSP-----VGL 225
                                                                                                                                    SPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 DFLLNYPFSTSVKLSTGCTG------TLVAEKHVLTAAHCIHDGKTYVKGTQK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C;Accession: S49075; JC4670; FS0191; PS0190; I62745
T;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
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                                                                                                                                                                                                                      SSSVTGFPCDKTFGTMWSDTKPIR-----SAETYKLTY-TTDTYGCQSGSPVY
                                                                                                                                                                                                                                                                                                                                                                                                -RNYSDTGQTAIAIHT------NGG-SSYNLGTRVTNDVFNNIQYW 310
                                                                                                                                                                                                                                                                                                             KRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 131; DB 2; Length 218;
Pred. No. 0.0021;
); Mismatches 87; Indels
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24.2%; Prective 30; 1
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Best Local Similarity 24.2%
Matches 59; Conservative
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A;Molecule type: DNA
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Accession: 140010
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Mocleaule vype: DNA
A.Residues: 1-60.65, L., 67, 8, 69, AQA, <RES.
A.Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702
A.Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702
R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A., A.; Azubano, V.; Carter, N.M.; Ch.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Ferrari, E.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Ferrari, E.
A.4 uthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Roetter, P.; Koningstefan, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Latulinois,
A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Lievine, A.; Liu, H.; Mauchors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Lievine, A.; Liu, H.; Mauchors: J.; Lazarevic, V.; Lee, S.M.; Lievine, A.; Liu, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A.Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seronakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpgtra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wippet, A.; Yamamac, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, F.
A.Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A.Reference number: Asserian P. Posser, M.; Bacillus subtilis.
A.Reference number: Asserian P. Posser, M.; Bacillus subtilis.
                                                                                                                                                                                                                                                                                           metalloproteinase (EC 3.4...) mpr precursor, extracellular - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 27-Jul-1990 #sequence.
C;Date: 27-Jul-1
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 GTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGD--GAQHRDSGSSGKSRRKRQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GCTGTL 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DGKTYVKGTQKLRVGFLKPKFKDGGRGAND 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STSAMPEQMKFQWIRVKRTHVPKGWIKGN---ANDIGMDYDYALLELKKPHKRKFMKIGV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 UNPNTWVTAGHCVYSQDHGWASTITAAPGRNGSSYPYGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Mismatches 121;
    344 QWVDMNGSPQDFNVAVRITPLKYAQICYW 372
                                                                                           ---SSYNRGTRITKEVFDNLTNW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: Glutamyl endopeptidase, V8 type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 VAEKHVLTAAHCIH------
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Best Local Similarity 22.2
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-313 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superramı.,.
C;Keywords: hydrolase
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A;Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are expl
A;Reference number: A90958; MUD:87217962; PMID:3646943
A;Recession: A26823
A;Molecule type: mRNA
A;Residues: 1-269 «KAW>
A;Cross-references: UNIPROT:P08419; GB:MI6651; NID:g164441; PIDN:AAA31027.1; PID:g164442
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-16/Domain: propeptide #status predicted «SIG>
F;17-28/Domain: signal sequence #status predicted «MAT>
F;29-569/Product: elastase II #status predicted «MAT>
F;29-262/Domain: trypsin homology «TRY>
F;39-262/Domain: trypsin homology «TRY>
F;31,121,216/Active site: His, Asp, Ser #status predicted
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A;Cross-references: UNIPROT:001771; EMBL:AF003134; PIDN:AAB54144.1; GSPDB:GN00019; CESP:?
A;Experimental source: strain Bristol N2; clone ZC581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 DIGMDYDYALLELKKP-HKRKFMKIGVSPPAKQ-LPG-----GRIHFSGYDND--R 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KLSTGCTGTLVAEK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 PPPLKILEMILYWLRIPPSAKVYNGRDASQSEAPWSVFTYLYSKDEQSATTCTGTIVSPR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 TYRVVLGRHSL-----STNEPGSLA-----VKVSKLVVHQDW---NSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 RVVGGEDARPN-----SWPWQVSLQYDSSGQWRHTCGGTLVDQSWVLTAAHCISSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TY--VKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 RQIYGYDSRFSIFGKDFLLNYPFSTSVKL-STG----CTGTLVAEKHVLTAAHCIHDGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.6%; Score 119; DB 2; Length 269; Best Local Similarity 27.5%; Pred. No. 0.027; Matches 60; Conservative 28; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 36/2; 138/3; 234/2; 311/1; 331/1; 421/1; 470/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 QGQLL-----VVD-----YATC-SKPGWWGSTVKTNM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 PGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRM 324
   R;Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y. DNA 6, 163-172, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein ZC581.6 - Caenorhabditis elegans
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Matches 95; Conserv
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C Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F; 1-23/Domain: signal sequence #status predicted <EGS>
F; 25-44/Domain: Data propertide #status predicted <EGS>
F; 1-179/Product: coagulation factor X light chain #status predicted <LCH>
F; 1-179/Product: coagulation factor X heavy chain #status predicted <HCH>
F; 1-179/Product: coagulation factor X heavy chain #status predicted <HCH>
F; 183-482/Product: coagulation factor X heavy chain #status predicted <ACT>
F; 222-482/Product: coagulation factor X heavy chain #status predicted <ACT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 183-186, X7,188-207 <ENJ2>
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Heematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of
A;Reference number: 146196; MUID:94222160; PMID:8168596
                                                                                                                                                     A. Accession: JC4670
A. Molecule type: mRNA
A. Rocession: JC4670
A. Molecule type: mRNA
A. Rocession: JC4670
A. Molecule type: mRNA
A. Rocession: JC4670
A. Rocession: JC4670
A. Experimental source: Cos-1 cell
A. Experimental source: Cos-1 cell
A. Experimental source: Cos-1 cell
A. Elochem. 109, 890-898, 1991
A. Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat E A. Reference number: PS0190; MUID:92041742; PMID:1718949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description: catalyzes the proteclytic activation of prothrombin to thrombin in the
A;Note: neither the complete nucleic acid sequence nor the complete translation are ER;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R. Scanton, C.; Ross, 1996
A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs. A;Reference number: JC4670; MUID:96194815; PMID:8647460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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N;Alternate names: pancreatopeptidase E
C;Species: Sus acrofa domestica (domestic pig)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: A26823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 CTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Molecule type: DNA
;Residues: 295-383, 'G',385-455 <MUR>
;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.7%; Score 120.5; DB 1; Length Best Local Similarity 32.3%; Pred. No. 0.041; Matches 31; Conservative 17; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 QWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 Q----RDŤY-------DFDIAMLRLKTP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: PS0191
A, Molecule type: protein
A, Residues: 41-58, 'X', 60-65 <ENJ1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: PS0190
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pancreatic elastase I (allele HEL1-16) probable splice form I - human C; Species: Homo sapiens (man)
C; Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 28-Apr-2003
C; Datesion: 307-312, 1992
R; Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.; DNA, Seq. 2, 303-312, 1992
A; Title: Genomic organization of the human homologue of the rat pancreatic elastase I ger A; Reference number: A56615; MUID:92338395; PMID:1633328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25528
R;Stevenaon, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II
A;Reference number: A93646; MUID:87066713; PMID:3641189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P05208; GB:X04573; NID:g50825; PIDN:CAA28242.1; PID:g50826 C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; serine proteinase F;1-30/Domain: signal sequence #status predicted <SIG>
                                                      11;
                                                                                                                   147 NYPFSTSVKLSTG-----CTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFK 200
                                                                                                                                                                                                                                         201 DGGRG----ANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP- 255
                                                                                                                                                                                                                                                                                                  --GRHNLYVAESGSLA-----VSVSKIVVHKDW---NSNQISKGNDIALLKLANPV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SNPGAGSAA-----VQVSKLVVHQRW---NSQNVGNGYDIALIKLASPVTLS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 YPFSTSVK-LSTG----CTGTLVAEKHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPKF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 KDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP-HKR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVKDETY----DLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 SVKSSMVCAGGDGVTSSCN---GDSGGPLNCRASNGQ---WQ--VHGIVSFGSSLGCN-Y 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic elastase II (EC 3.4.21.71) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 KFMKIGVSPPAKQ-LPGGRI-HFSGY------DNDRPGNLV---YRFC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 SWPWQVSLQYSSNGKWYHTCGGSLIANSWVLTAAHCISSSRTY------RVGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     256 HKRKFMKIGVSPPAKQ-LPG------GRIHFSGYDND--RPGNLV---YRFC 295
                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.1-30/Domain: signal sequence #status predicted <SIG>F.31-271/Product: pancreatic elastase II #status predicted <MAT>F.31-264/Domain: trypsin homology <TRY>F.35.123,218/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.4%; Score 115.5; DB 2; Best Local Similarity 25.0%; Pred. No. 0.053; Matches 67; Conservative 38; Mismatches 80;
                         0.052;
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQDFNVAVRITPLKYAQICYWIKGNYLD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NYID 262
                         Pred. No.
28.6%; FIL.
                                                      50; Conservative
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PRKPSVFTRVS---
                   Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-271 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A25528
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A;Molecule type: mRNA
A;Redideus: 1-269 «KMA»
A;Cross-references: UNIPROT:P08217; GB:M16652; NID:g182057; PIDN:AAA52380.1; PID:g182058
R;Fletcher, T.S.; Shen, W.F.; Largman, C.
Biochemiatry 26, 7256-7261, 1987
A;Title: Primary structure of human pancreatic elastase 2 determined by sequence analysi
A;Reference number: A27432; MUID:88107669; PMID:3427074
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, Residues: 1-269 «FLE»
, Gross-references: GB.M16631; NID:g182022; PIDN:AAA52374.1; PID:g182023
, Shirasu, Y.; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, T.
Biochem. 102, 1555-1563, 1987
. Biochem. 102, 1555-1563, 1987
. Title: Molecular cloning and expression in Escherichia coli of a cDNA encoding human ; Reference number: A41431; MUID:88198076; PMID:2834346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNAs are
                                                                                                                                                                                                                                                                                                                                     306 SVCVADDETQPNDKLSLEYFGFGLNPPSD-----INQNGVDN--TGQLRYEKIEVFRSH 357
                                                                                                                                                                                                                                      -KGISRYPEKITLVHACTKRT-----ANRTKKIPPOYYTDDFAIVHLYEELTFSSNVQ 305
                                                                                                                                                                                                                                                                                                  ------KKPHKR---KFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY----- 292
                                                                                                                                                                                                                                                                                                                                                                                                                            -----RECDVKDETYD-----LLYQQCDAQ----PGASGSGVYVRMWKRQQQKWE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 PMEIYFFQARDITDKTVACVVSLKILILNKTQASLNISLKGDSGGAIADV-----KGK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Homo sapiens (man)

Date: 16-Aug-1988 #sequence revision 16-Aug-1988 #text_change 09-Jul-2004
Accession: B26823; A27432; Ā41431; S34491
Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
NA 6, 163-172, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA 6, 163-172, 1987
A;Title: Characterization of pancreatic elastase II cDNAs: two elastase II
A;Reference number: A90958; MUID:87217962; PMID:3646943
                                                                                                            202 HILIATHCFAGONRDGSWNLIEDTFDRSNCKDDDYVITNOEFLKRVEFLSNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-201, VV, 203-269 <SHI>
A; Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1; PID:g219620
A; Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1; PID:g219620
A; Noce: the authors translated the codon GTG for residue 202 as Cys
R; Moulaci, M.; Michon, T.; Kerfelec, B.; Chapus, C.
FEBS Lett. 261, 179-183, 1990
A; Title: Further studies on the human pancreatic binary complexes involvi
A; Reference number: S08253; MUID:90169111; PMID:2307232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Map position: 12pter-12qter;
Superfamily: trypsin; trypsin homology
Keywords: hydrolase; pancreas; serine proteinase;
1.16/Domain: signal sequence #status predicted <8IG>
1.29.26/Product: pancreatic elastase IIA #status predicted <MAT>
1.29.26/Product: pancreatic elastase IIA #status predicted <MAT>
1.20.26/Domain: trypsin homology <TRY>
1.21,216/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 RKIIGIFS-----GHQWVDMNGSPQDFNVAVRITPLKYAQIC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 NDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDY---DYALLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pancreatic elastase II (EC 3.4.21.71) A precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 115.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S34491
Molecule type: protein
Residues: 'X',18-50 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
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A; Reference number: S19890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Genetics:
A,Gene: SP0390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A56615; S70440 — R;Kawashima, I.; Tani, T.; Furukawa, H R;Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H A;Tatle: Ganomic organization of the human homologue of the rat pancreatic elastase I A;Reference number: A56615; MUID:92338395; PMID:1633328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin-like proteinase (EC 3.4.21.-) 5G1 precursor - yellow fever mosquito (fragment)
C,Species: Aedes aegypti (yellow fever mosquito)
C,Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rikalhok, S.; Tabak, L.M.; Prosser, D.E.; Downe, A.E.R.; White, B.N. submitted to the EMBL Data Library, Pebruary 1992
A;Description: Isolation, sequencing and characterization of 2 cDNA clones coding for
                                                                                                                                                                                             9
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                                                                                                                                                                                                                                        147 NYPFSTSVKLSTG-----CTGTLVAEKHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
                                                                                                                                                                                                                                                                                                                                      199 FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
                                                                                                                                                                                                                                                                                                                                                                    147 NYPFSTSVKLSTG-----CTGTLVAERHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
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                                                                                                                                                                                                                                                                    SWPSQISLQYRSGGSWYHTCGGTLIRQNWVMTAAHCVDYQKTFRVVAGDHNL-----
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                                                                                                                                                                                           34;
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A, Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable pancreatic elastase (EC 3.4.21.36) pseudogene - human
                                                                                                                                                                                           38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
               A;Molecule type: DNA
A;Residues: 1-258 <KAM>
A;Note: it is not known whethere the gene is expressed
F;19-251/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: hydrolase; pseudogene; serine proteinase
                                                                                                                                           Score 115; DB 4
Pred. No. 0.055;
                                                                                                                                                                                        23, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Mismatches
                                                                                                                                           Query Match'
Best Local Similarity 26.9%;
Matches 35; Conservative 2:
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124 NSYVQLGVLP 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: A56615
A,Molecule type: DNA
A,Residues: 1-267 <KAW>
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Best Local Similarity
Matches 35; Conserv
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A;Map position: 12
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A;Cross-references: UNIPROT:Q97SH5; GB:AE005672; PIDN:AAK74556.1; PID:g14971860; GSPDB:G}
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: C95045
R;Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Accession: C95045
A, Accession: S19891
A, Molecule type: mRNA
A, Residues: 1-238 «KAL»
A, Cross-references: UNIPROT: P29787; EMBL: X64363; NID: 95563; PIDN: CAA45715.1; PID: 95564
C, Superfamily: trypsin; trypsin homology
C, Keywords: Hydrolase, insect midgut, protein digestion; serine proteinase
F;1-11/Domain: signal sequence and propeptine (fragment) #status predicted «SIG»
F;12-238/Product: trypsin-like proteinase 5G1 #status predicted «MAT»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 PFSTS----VKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 ------QLIKVKKVNRHPK-----YDEVTTDYDFALIELEETVTFSDSCAP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 ANDSTSAMPEQMKFQWIRVKRTH-VPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              choline binding protein G [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 PPQVSLSGVGSSHFCGGSLLSERWVMTAGHCAASGQTNL----QVRIG--SSQHASGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 TGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGAND---STSAMPEQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 HFSGYDNDRPGNLVYRF-----CDVKDETYD---LLYQQCDAQPGASGSGVYVRMWKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SANFIKDNVLITAAH-----NYYR-------HDYGKEADDIYVLPAVSPSQE
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                                                                                                                                                                                                                                                                                     F:12-232/Domain: trypsin homology <TRY>
F:38-54,162-178,189-213/Disulfide bonds: #status predicted
F:53,97,193/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 114.5; DB
Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.4%; Score 114.5; Best Local Similarity 29.4%; Pred. No. 0.05 Matches 42; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 VKLPQKDTPVNEGTCLQVSGWGN 138
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Best Local Similarity 23.4%;
Matches 54; Conservative 3
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C;Accession: JS0013; A26777; A10061; A00959
R;Shirasu, Y.; Yoshida, H.; Mikayama, T.; Matsuki, S.; Tanaka, J.I.; Ikenaga, H.
J. Biochem. 99, 1707-1712, 1986
A;Title: Isolation and expression in Bscherichia coli of a cDNA clone encoding porcine parkeerence number: A92005; MUID:86304235; PMID:3528137
A;Accession: JS0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 1-125,'G',127-183,'L',185-266 <TAN>
A,Residues: 1-125,'G',127-183,'L',185-266 <TAN>
A,Cross-references: GB:D00160; NID:g217683; PIDN:BAA00118.1; PID:g217684
A,Note: the authors translated the codon GGG for residue 58 as Gln, GGC for residue 126 & R;Shotton, D.M.; Hartley, B.S.
Biochem. J. 131, 643-675, 1973
Biochem. J. 131, 643-675, 1973
A,Fitle: Evidence for the amino acid sequence of porcine pancreatic elastase.
A,Reference number: A90267; MUID:73229121; PMID:4578945
                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-266 <SHI>
A;Cross-references: UNIPROT:P00772; GB:X04036; GB:D00070; GB:N00070; NID:g1941; PIDN:CAA;
B;Tani, T.; Kawabhima, I.; Furukawa, H.; Ohmine, T.; Takiguchi, Y.
J. Biochem. 101, 591-599, 1987
A;Title: Characterization of a silent gene for human pancreatic elastase I: structure of A;Reference number: A26777; MUID:87250343; PMID:3648024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dancreatic elastase (BC 3.4.21.36) I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Bate: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A009560; A20534
R;MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Ruttes
Biochemistry 21, 1455-1463, 1982
A;Title: Primary structure of two distinct rat pancreatic preproelastases determined by & A;Reference number: A00960; MUID:82182967; PMID:6918221
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A;Cross-references: UNIPROT:P00773; GB:V01234; NID:g56088; PIDN:CAA24544.1; PID:g56089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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A;Cottents: annotation; X-ray vistallography, 3.5 angstroms; active site C;Superfamily: trypsin; trypsin; homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen
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F;17-26/Domain: activation peptide #status predicted <APT>
F;27-266/Product: elastase I #status experimental <MAT>
F;27-256/Domain: trypsin homology <TRY>
F;26-7259/Domain: trypsin homology <TRY>
F;56-72,153-220,184-200,210-240/Disulfide bonds: #status experimental
F;71,119,214/Active site: His, Asp, Ser #status experimental
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A,Title: Isolation and characterization of rat pancreatic elastase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 27-91,'N', 93-203,'N', 205-266 <SHO>
R;Shocturo, D.M.; Hartley, B.S.
Nature 225, 811-816, 1970
A,Title: Three-dimensional structure of tosyl-elastase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22, 3763-3770, 1983
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Matches 36; Conservative
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                                                                                  complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
NyAlternate names: adipsin; C3 convertase activator
C;Species: Homo sapiens (man)
C;Dete: 28-Aug-1985 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40197; A00936; A60571; S66645
E;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.; J. Biol. Chem. 267, 9210-9213, 1992
A;Title: Human adipsin is identical to complement factor D and is expressed at high leve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 19-44, 'G', '46-51, 'Q', 53-75, 'TH', '78, 'P', 80-83, 'XXXITIE', 90-172, 86-91, 185-235, 'A; Residues: 19-44, 'G', '46-51, 'Q', 53-75, 'TH', '78, 'P', 80-83, 'XXXITIE', 90-172, 86-91, 185-235, 'A; Note: a few residues were assigned from the previoually published sequence of Reid et a R; Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya Mol. Immunol. 27, 637-644, 1990
A; Title: Molecular and functional identification and purification of complement component A; Reference number: A60571; MUID: 90370044; PMID: 2395435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Status: preliminary
;Molecule type: protein
;Residues: 19-44,′C′,46-48 <BAL>
;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
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C; Superfamily: trypsin, trypsin homology
C; Superfamily: trypsin, trypsin pathway; hydrolase; plasma; serine proteinase
C; Keywords: complement electrate pathway; hydrolase; plasma; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-246/Product: complement factor D (fragment) #status experimental <NAT>
F;19-241/Domain: trypsin homology <TRX>
F;19-241/Domain: trypsin homology of Signal #status predicted
F;59,105,201/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:P00746; GB:M84526
R;Niemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 31, 248-2486, 1984
A;Title: Anino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 PFSTSVKLSTG--CTGTLVAEKHVLTAAHCIH---DGKTYVKGTQKLRVGFLKPKFKDGG
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28.4%; Pred. No. 0.062;
ative 20; Mismatches 4
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A; Molecule type: mRNA
A; Residues: 1-246 < WHI>
A; Cross-references: UNIPR
R; Niemann, M.A.; Bhown, A
Biochemistry 23, 2482-248
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Q6AZC0
Q9GMD9
                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                          UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                             US-09-658-677-15
2131
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Match Length DB
                                                       July
                                                                                             Title:
Perfect score:
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131
129.5
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127.5
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1888.5
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1042
1016.5
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1005.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
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 121
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                     Carausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schmit J., Jones S.J.M., Marra M.A.,
H. Generation and initial analysis of more than 15,000 full-length human
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100.0%; Pred. No. 1.3e-167;
iive 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                            Proc. Nall. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the peptidase S1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF015287; AAD01553.1; --
EMBL; AF193611; AAF07186.1; --
EMBL; AL13694; CAB66848.1; --
EMBL; AX359033; AAQ83992.1; --
EMBL; BC001278; AAH01278.1; --
MEROPS; S01.309; --
H-InvDB; HIX001006; --
                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
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TISSUB-Kidney,

TISSUB-Kidney,

TISSUB-Kidney,

PubMed=12477932; DOI=10.1073/pnas.242603899;

Rataubberg R.L., Feingold B.A., Grouse L.H., Schamen C.M., Schuler G.D.,

RIausner R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

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Brownstein M.J., McKernan K.J., Malek J.A., Gubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rah, Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ray Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
                                                             240
                                                                                                                                                           300
                                                                                                                                                                                                                                                        360
SGKSRRKRQIYGYDSRFSIFGKDFLLNYPPSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
                                                                                                            240
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                                                                                                                                                                                                                                                                                 GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
GO; GO:0006334; P:nucleosome assembly; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                           KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                  KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                                                             241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                        241 IGMDYDYALLELKKPHKRKFWKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                        TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB-Kidney,
Director MGC Project,
Submitted (MGC-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL, BC079179; AAH79179.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 AA
                                                                                                                                                                                                                                                                                                                                                      ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                                                                                                                                                              361 ITPLKYAQICYWIKGNYLDCREG 383
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61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSNGEGRARSRDSEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VSSSCGPQCHKGTPLPTYBEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=C57BL/63; TISSUE=Tongue;

X MEDILINE=25154668; PubMed=12466851; DOI=10.1038/nature01266;

A Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

A Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Balla E., Dragani T.A., Pletcher C.F., Forrest A., Frazer K.S.,

RA Balla E., Dragani T.A., Fletcher C.F., Forrest R., Frazer K.S.,

RA Gasererland T., Garuboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAGIPGLLILLLVILCVFMQVSPYNVPWKPTWPAYRLPIVLPQSTLKLAKPDFDAKAKLE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                              Query Match 89.3%; Score 1903; DB 2; Length 383; Best Local Similarity 91.4%; Pred. No. 1.3e-152; Matches 350; Conservative 11; Mismatches 22; Indels
                                                                                                                                                                                                                               protease
                                                                Pfam; PP00089; Trypsin; 1.
PRINTS; PR00722; CHYMORRYPSIN.
ProDom; PD001827; Histone H4; I.
PROSITE; PS00134; TRYPSIN H1S; UNKNOWN 1.
Hydrolase; Hypothetical protein; Protease; Serine protesseguence 383 AA; 43159 MW; 4AB12CC7B66CDFC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9D6X6; Q8VEG1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
5-CCT-2004 (Rel. 45, Last annotation update)
Serine protease 23 precursor (EC 3.4.21.-).
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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M., Takenaka Y., Taylor M., Takenaka Y., Taylor M., Takenaka Y., Taylor M., Takenaka Y., Watanabe Y., Walla K., Wang Y., Watanabe Y., Walla C., Wynshaw-Boris A., Yanagisawa M., Yang I., This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). similarity).
similarity).
similarity). (Potential). ~ . and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the peptidase S1 family. Serine protease 23.
Charge relay system (I Charge relay system (I Charge relay system (I By similarity. PEAM; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp. SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; FALSE NEG.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; FALSE NEG.
Hydrolase; Serine protease; Signal. Potential. EMBL; AK009847; BAB26541.1; -EMBL; AK078518; BAC37319.1; -EMBL; BC018517; AAH18517.1; -HSSP; P00746; IDSU.
HSSP; S01.309; -MGD; MGI:1923703; 2310046G15Rik.
INTERPRO; IPR009003; Pept Ser Cys.
INTERPRO; IPR001254; Peptidase_S1.
INTERPRO; IPR001314; Peptidase_S1. 420:563-573 (2002) tumor; SEQUENCE FROM N.A. TISSUE=Breast ACT_SITE ACT_SITE ACT_SITE DISULFID SIGNAL CHAIN

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                                                                         1:
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                                                                                                                                                            60 VSSSCGPQCHKGIPLPTYEEAKQYLSYETLYANGSRIETRVGIYILSNGEGRARGRDSEA 119
                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                            180 KTYVKGTQKLRVGFLKPKYKDGAGGDNSSSSAMPDKMKFQWIRVKRTHVPKGWIKGNAND 239
                                                                                                                                             61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                           301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                                                                                                                                                                                                                                     359
                                                                                                 9
                                                                                                               1 MAGIPG-LFILLVLLCVFMQVSPYTVPWKPTWPAYRLPVVLPQSTLNLAKADFDAKAKLE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Cecum;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Hanalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                              121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
                                                                                                                                                                                                                                                                                                          240 IGMDYDYALLELKKPHKRQFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                                                                                                                           MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
                                                                                                                                                                                                                                               181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
                                                                                                                                                                                                                                                                                             241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUB=Cecum; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male cecum cDNA, RIKEN full-length enriched
library, clone:913015B18 product:SERINE PROTEASE (HYPOTHETICAL 43.0
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
N-linked (GlcNAc. .) (Potential).
M -> I (in Ref. 1; BAB26541).
6F09A5C80A5B2306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                         1;
                                                 DB 1; Length 382;
                                             Query Match

88.6%; Score 1888.5; DB 1; Length
Best Local Similarity 90.9%; Pred. No. 2.1e-151;
Matches 348; Conservative 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUE=Cecum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AA
                                                                                                                                                                                                                                                                                                                                                                                                         360 ITPLKYAQICYWIKGNYLDCREG 382
                                                                                                                                                                                                                                                                                                                                                                                           361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                         43071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
206
260
382 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria
NCBI_TaxID=10090;
CARBOHYD
CONFLICT
                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8BZS4
Q8BZS4;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashlaume W., Haramoto K., Haraharama T., Haraharama T., Haraharama T., Hayashida K., Hayatsu M., Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T., Atoch H., Kawai J., Kojima Y., Kondo S., Konno H., Koda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nakamura M., Salto H., Sakai C., Sakai K., Ohno M., Ohasto N., Okazaki Y., Salto R., Saitoh H., Sakai C., Sakai K., Sakaume N., Sano H., Salto R., Shibata K., Shinagawa A., Shiradaw T., Takkul-Akahira S., Takeda Y., Takau A., Buramatsu M., Hayashizaki Y., Takau J., Takau J., Muramatsu M., Hayashizaki Y., Takau J., Takau J., Muramatsu M., Hayashizaki Y., Takau J., Saitoh J., Takau J., Gangawa A., Takahashi F., Takau J., Muramatsu M., Hayashizaki Y., Takau J., Jaka J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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[4]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cecum;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETRVGIYILSNGEGRARGRDSEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUCDANCE FROM N. A. SUBE-Cecum,
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Mishiara K., Itoch M., Aizawa K., Magaoka S., Sasaki N., Carninci P., Sumin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RTKBN Integrated sequence analysis (RISA) system=384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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SEQUENCE 382 AA; 43147 MW; 556789818E12A081 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.6%; Pred. No. 6.8e-151;
:ive 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.68
Matches 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altauner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boak S.A., McKernan R.J., Malke J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human
296 SPIIKKMPGGMIHFSGFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLK 355
                                                                              326 KRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLDCREG 383
                                                                                                            356 DPDKKGWWKRKIIAVYSGHQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=22807296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                         Name-PRSS15; ORFNames-UNQ522;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:trypsis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
02-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical proctein PRSS35 (ENMLS22).
Name-PRSS35; ORFNames=UNQ522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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EMBL; BC037170; AAH37170.1; -.
EMBL; AY358661; AAQ89024.1; -.
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                                                                                                                                                                                                                                                                    413
                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bioinformatics assessment.
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=9606;
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                                                                                                                                                                                                                                                                      300 TYDLLYQQCDAQPGASGSGVYVRMWKRPQQKWERKIIGIFSGHOWVDMNGSPODFNVAVR 359
                                240 IGMDYDYALLELKKPHKRQFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 299
                                                                                                       301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 CGIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPT-----QNITTKG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 VSVRRKRQVYGTDSRFSILDKRFLINFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 SPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LLFLLFFLLCAVG--QVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 KS-RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 TYVKGTQKLRVGFLKPKFKDGGR------GANDSTSAMPEQMK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 48.9%; Score 1042; DB 2; Length 4 Best Local Similarity 47.8%; Pred. No. 1.1e-79; Matches 200; Conservative 68; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; AL121939; CAC35071.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERNTS; PROOFER, Trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
Hydrolase; Protease; Serine protease.
SEQUENCE 413 AA; 47098 MW; 818D9C951BD2D6C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew, HGNC.21387; PRSS35.

Genew, HGNC.21387; PRSS35.

GO: GO:0004236; F:CHYPGIN activity; IEA.

GO: GO:0004239; F:Peptidase activity; IEA.

GO: GO:0004295; F:trypsin activity; IEA.

GO: GO:0006508; P:proteclysis and peptidolysis; IEA.

InterPro; IRR001234; Peptidase S1.

InterPro; IRR001314; Peptidase S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DJ22311 (Putative secreted protein ZSIG13).
Name=dJ223183.1;
                                                                                                                                                                                                              361 ITPLKYAQICYWIKGNYLDCREG 383
                                                                                                                                                                                                                                           360 ITPLKYAQICYWIKGNYLDCREG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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09BQP6
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                                                                                                                                                                                                                                                                                                                                                 CGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGI--YILSSSGDGAQHRDSGSSG 122
                                                                                                                                                                                                                                                                                                                                                                                                                               123 KS-RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 SPIIKKWPGGMIHPSGPDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLK 355
                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                      182 TYVKGTOKLRVGFLKPKFKDGGRGANDSTSAMPE-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/61; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030424L22 product:similar to DJ223B3.1
(PUTATIVE SECRETED PROTEIN ZSIG13), full insert sequence (Protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                              50;
                                                                                                                                                                                  48.9%; Score 1041; DB 2; Length 413; 47.8%; Pred. No. 1.4e-79;
                                                    Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Hypothetical protein; Protease; Serine protease.
SEQUENCE 413 AA; 47070 MW; 2D43814519030SC0 CRC64;
                                                                                                                                                                                                                            Indels
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                          68; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 AA.
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01-MAR-2003 (TrEMBLrel. 23, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
IPR001254; Peptidase_S1.
IPR001314; Peptidase_S1A.
IPR009003; Pept_Ser_Cys.
                                                                                                                                                                                                Best Local Similarity 47.8% Matches 200; Conservative
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01-MAR-2003
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                                            InterPro;
  InterPro;
                    InterPro;
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 88 FENGTRILIRUKVQQLVLEPTRNSSVKGAH------PRRRRQVYGTDSRFSILDKRF 138
 318
 199 KRRGSKRSRREAESAGQSQAHLRESTTQRPGKKSRRGPRVTQGRPSFQWTRVKSTHIPKG 258
 319 RFCSVSEESNDLLYQYCDAEAGSTGSGIYLRKEPGQKNWKRKIVAVYSGHQWVDVHGVQ 378
 233 WIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY 292
 293 RFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSP 352
 28 TWHLSRIPQVVSENTIHLASPTFQADAGVVKATVCGIECQEELPAPSLSQLEESLSYETI 87
 145 LLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDG--
 31 TWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLPTYEEAKQYLSYETL
 203 -GRGA-----KFQWIRVKRTHVPKG
 TISSUE-Whole;
MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Mooret T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 91 YANGSRIETQVGIYIL------SSSGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDF
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
 47;
 Query Match

47.7%; Score 1016.5; DB 2; Length 409;
Best Local Similarity 49.4%; Pred. No. 1.6e-77;
Matches 193; Conservative 68; Mismatches 83; Indels 47;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: Belongs to peptidase family S1.

EMBL; BC075675; AR475675.1; -..

MGD; MGI:2444800; Pr8935.

GG; GG:0605615; C:extracellular space; TAS.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR00903; Pept Ser_Cys.

Pfam; PF00089; Trypsin; 1.

RMRT; SM00020; Trypsin; 1.

RMRT; SM00020; Tryp SPC; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.

Hydrolasse; Proteases: Serine protease.

SEQUENCE 409 AA; 45787 MW; 6E22D4A908E7EFE5 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 379 KDYNVAVRITPLKYAQICLWIHGNAANCAYG 409
 353 QDFNVAVRITPLKYAQICYWIKGNYLDCREG 383
 Brachydanio rerio (Zebrafish) (Danio rerio).
 418 AA
 PRT;
 PRELIMINARY;
 ORFNames=zgc:91804;
 SEQUENCE FROM N.A.
 Cyprinidae, Danie
NCBI_TaxID=7955;
 Zgc:91804.
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 262 KIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVY 321
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernen K.J., McKernen K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 LHGICGIECQQRLPEPSLDDLEQLLSYETWYDNGTRTLTTVTVQDLNVSNDWT----GAS
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 177 TDYLDGVQKLSVGVLKERSRRKNGRKGKGRKGKGQRKHEEEEEVDENGEIVEKQQERKSKG
 202 GGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFM
 322 VRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLDCR
 Gaps
 43;
 47.6%; Score 1014.5; DB 2; Length 418; 46.6%; Pred. No. 2.4e-77; Live 64; Mismatches 118; Indels 43;
 TISSUE-Whole;
Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC074028; AAH74028.1; -.
ZFIN; ZDB-GENE-040704-55; zgc:91804.
ZGO:0008233; F:peptidase activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
InterPro; IFR001254; Peptidase S1.
InterPro; IFR001254; Peptidase S1.
InterPro; IFR001254; Peptidase S1.
 Pfam; PF00089; Trypsin; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 418 AA; 47270 MW; AF53345CEE94F720 CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 409 AA.
 181 KTYVKGTQKLRVGFLKP------
 QBCOL5 PRELIMINARY; PRT; QBCOL5; (TrEMBLrel. 23, Created)
 Best Local Similarity 46.68
Matches 196; Conservative
 mouse cDNA sequences.
 SEQUENCE FROM N.A.
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 STRAIN-CSTRU, G.; TISSUE-Head;
A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rudda S., Purnon M., Hanagaki T., Hara A., Hashizume W., Purnon M., Hanagaki T., Hara A., Hashizume W., Hayatsu W., Hiracka T., Hiracka T., Hiracka T., Hiracka T., Hiracka T., Hiracka T., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Koya S., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito H., Sato H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

E EMBL, AKOSOGTI; BACZZOGTI; ---
E SIMILARITY: Belongs to peptidase family SI.
 SEQUENCE FROM N.A.
STRAINE-STRBL/GJ; TISSUE=Head,
The FANTOM CONSORTING.
The RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
 STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Shibata K., Itoh M., Formalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279255; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 STRAIN=C57BL/Gj; TISSUE=Head; MEDLINE=26530913; Pubmed=11076661; DOI=10.1101/gr.152600; Shibate K., Itoh M., Aizawa K., Negaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Masuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKIXI integrated sequence analysis (RISA) system 384-format
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
library, clone:943041704 product:similar to DJ223E3.1 (PUTATIVE
SECRETED PROTEIN ZSIG13), full insert sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 "Functional annotation of a full-length mouse cDNA collection.";
 STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 Genome Res. 10:1757-1771(2000)
 Nature 409:685-690(2001).
 RIKEN FANTOM Consortium;
 EMBL; AK030671; BAC27073
MGD; MGI:2444800; Prss35
 (Mouse)
 FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Mus musculus
 Name=Prss35;
 SEQUENCE
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 88 FENGTRILIRVKVQGLVLEPTRNSSVKGAH-----PRRRRQVYGTDSRFSILDKRF 138
 258
 144
 232
 292
 RFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSP 352
 90
 87
 28 TWHLSRIPQVVSENTIHLASPTFQADAGVVKATVČGIEČQBELPAPSLSQLEESLSYETI
 31 TWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLPTYEEAKQYLSYETL
 91 YANGSRIETQVGIYIL----SSSGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDF
 145 LLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDG--
 -----NDSTSAMPEQM------KFQWIRVKRTHVPKG
 199 KRRGSKRSRREAESAGOSOAHLRESTTORPGKKSRRGPRVTOGRPSFOWTRVKSTHIPKG
 WIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY
 STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MUS musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030466M24 product:similar to DJ223E3.1
(PUTATIVE SECRETED PROTEIN ZSIG13), full insert sequence.
 47;
 DB 2; Length 409;
 47.5%; Score 1011.5; DB 2; Length
49.1%; Pred. No. 4.2e-77;
tive 68; Mismatches 84; Indels
 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 PEAM, PF00089; Trypsin; 1.
PRINTS, PR00722; CHYMOTRYPSIN.
SMART, SM0020; Tryp.SPC; 1.
PROSITE; PS00134; TRYPSIN HS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 409 AA; 45847 MW; A5ACIC582BFD352E CRC64;
 Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 QDFNVAVRITPLKYAQICYWIKGNYLDCREG 383
 ż
GO:0005615; C:extracellular space; TAS
 409
 InterPro, IPR001254; Peptidase Sl.
InterPro, IPR001314; Peptidase_SlA.
 PRT;
 InterPro; IPR009003; Pept Ser Cys
 Matches 192; Conservative
 PRELIMINARY;
 RIKEN FANTOM Consortium;
 203 -GRGA----
 Local Similarity
 SEQUENCE FROM N.A.
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 Name=Prss35;
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 199 KRRGSKRSRREAESAGOSQAHLRESTTORPGKKSRRGPRVTOGRPSFOWTRVKSTHIPKG 258
 STRAIN=ATCC 14580;

MEDLINE=30504737; PubMed=1429718;

Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E.,

Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N.;

"Purification, characterization, cloning, and expression of a glutamic

"Purification, characterization, cloning, and expression of a glutamic

acid-specific procease from Bacillus licheniformis ATCC 14580.";

J. Biol. Chem. 267:23782-23788 (1992).
 RFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSP
 WIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY
 -!- CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-Xaa, Glu-|-Xaa.
 01-MAY 1992 (Rel. 22, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Glutamyl endopeptidase precursor (BC 3.4.21.19) (Glutamate specific
endopeptidase) (GSE).
 -!- SUBCELLULAR LOCATION: Secreted.
 Pfam; PF00089; Trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00672; V8 HIS; 1.
PROSITE; PS00673; V8 SER; 1.
Direct protein sequencing; Hydrolase; Serine protease; Signal.
 Bacillus licheniformis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus
 353 QDFNVAVRITPLKYAQICYWIKGNYLDCREG 383
 316 AA
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
 PRT;
 InterPro; IPR000126; Pept_SIB_AS.
InterPro; IPR009003; Pept_Ser_Cys.
InterPro; IPR001254; PeptIdase_SI.
InterPro; IPR008256; Peptidase_SIB.
 EMBL; D10060; BAA00949.1; -.
PIR; A45134; A45134.
 STANDARD;
 NCBI TaxID=1402;
 MEROPS; S01.271;
 Name=blaSE;
 GSEP_BACLI
 319
 293
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 138
 A Adachi J. Aizawa K., Atimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Atimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Atimura T., Hara A., Hashizume W., Hirozane T., Harabachida K., Hayateun W., Hirachoto K., Hiracka T., Kasukawa T., A Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., A Katoh H., Kawai J., Kojima Y., Kohdo S., Komno H., Kouda M., Koya S., Kurhara C., Matsuyama T., Muyazaki A., Murata M., Nomara K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Salazuma N., Sano H., Salato R., Salton R., Shibata K., Shinagwa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Taya K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (Jul. 2001) to the EMBL/GenBank/DDBJ databases.
 144
 ---NDSTSAMPEQM------KFQWIRVKRTHVPKG 232
 90
 87
 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
 STRAIN=C57BL/6J; TISSUE-restis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 FENGTRILTRVKVQGLVLEPTRNSSVKGAH------PRRRRQVYGTDSRFSILDKRF
 91 YANGSRTETQVGIYIL-----SSSGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDF
 145 LLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTOKLRVGFLKPKFKDG--
 TWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLPTYEEAKQYLSYETL
 Gaps
 MEDLINE-257BL/60; TISSUE-Testis;
MEDLINE-257BL/60; TISSUE-Testis;
MEDLINE-257BL/60; TISSUE-Testis;
MEDLINE-257BL/60; TISSUE-TESTIO-1005BL/60; Sasaki N., Carninci P., Solibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Sequencing pipeline with 384 multicapillary sequencer.";
 47;
 409;
 47.2%; Score 1005.5; DB 2; Length 48.8%; Pred. No. 1.4e-76; ive 70; Mismatches 83; Indels
 45736 MW; E9C9B91E6800719C CRC64;
 MGD; MGI:2444800; Pr8835.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR009003; Pept_Ser_Cys.
 protease
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM CONSOrtium,
 Genome Res. 10:1757-1771 (2000)
 SMART; SM00020; Tryp_SPc; 1.
Hydrolase; Protease; Serine I
 Pfam; PF00089; Trypsin; 1.
 Conservative
 -GRGA----
 409 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
 191;
 SEQUENCE
 28
 203
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 Query Match
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Matches
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Serine protease, putative.
OrderedLocusNames=LMO£2365_
 Best Local Similarity 24.08
Matches 79; Conservative
 PRELIMINARY;
 SMART; SM00728; ChW; 3
 NCBI_TaxID=265669;
 Q71YES;
05-JUL-2004
 Hydrolase.
 SEQUENCE
 Query Match
 Q71YES
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 170
 80 KAEKKSPAKAPY---SIKSVIGSDDRTRVTNTTAYPYRAIVHISSSIGSCTGWMIGPKTV 136
 171 LTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHV 229
 137 ATACHCIYDTSSGSFAGTATVSPG------RNGTS-----YPYGSVKSTRYFI 178
 230 PKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGN 289
 290 LVYRFCD---VKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKII-----GIFSGH 343
 234 TQWQHSGPIAISETYKLQYAM-DTYGGQSGSPVFEQSSSRTNCSGPCSLAVHTNGVYGG- 291
 79
 "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:877-877(2004).
EMBL; AR017333; AAU39298.1; -.
 63 SSCGPQCHKGTPL---PTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSG
 28 AQAAPSPH--TPVSSDPSY-KAETSVTYDP-----NIKSDQYGLYSKAFTGTGKVNETKE
 120 SSGKSRRKRQIYGYDSRFSIFGKDFLLN-----YPFSTSVKLST---GCTGTLVAEKHV
 9.1%; Score 194; DB 1; Length 316;
24.0%; Pred. No. 5.2e-08;
ative 43; Mismatches 143; Indels 64; Gaps
 SEQUENCE FROM N.A.
STRAIN-ATCC 14580;
STRAIN-ATCC 14580;
FREY M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky B.J.
Tang M., de Leon A.L., Xiang H., Gueti V., Clausen I.G., Olsen P.B.
Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
 ä
 Glutamyl endopeptidase.
Charge relay system (By similarity)
Charge relay system (By similarity)
 Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottechalk G.; "The Complete Genome Sequence Of Bacillus licheniformis DSM13, Organism with Great Industrial Potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
 25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Mpr (EC 3.4.21.19) (Glutamyl Endo peptidase).
Mame=mpr; OFFNames=BLO1804, BLi00340;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacilluscae; Bacillus.
 33611 MW; 96D7552CB7089B09 CRC64;
 PRT; 316 AA
 344 QWVDMNGSPQDFNVAVRITPLKYAQICYW 372
 -----SSYNRGTRITKEVFDNLTNW 311
 Potential
 Conservative
 PRELIMINARY;
 30
316
141
141
142
279
 Query Match
Best Local Similarity
 141
261
126
275
316 AA;
 SEQUENCE FROM N.A.
 PubMed=15383718;
 STRAIN=DSM 13;
 ACT_SITE
ACT_SITE
DISULFID
 292
 SEQUENCE
 DISULFID
 Q65NR6
Q65NR6;
SIGNAL
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63 SSCGPQCHKGTPL---PTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSG 119
 137 ATAGHCIYDTSSGSFAGTATVSPG-----RNGTS-----YPYGSVKSTRYFI 178
 80 KAEKKSPAKAPY---SIKSVIGSDDRTRVTNTTAYPYRAIVHISSSIGSCTGWMIGPKTV 136
 :: | :: | :: | :: | 334 TOWOHSGPIAISETYKLOYAM-DTYGGOSGSPVPEQSSSRTNCSGPCSLAVHTNGVYGG- 291
 28 AQAAPSPH--TPVSSDPSY-KAETSVTYDP-----NIKSDQYGLYSKAFTGTGKVNETKE
 120 SSGKSRRKRQIYGYDSRFSIFGKDFLLN-----YPFSTSVKLST---GCTGTLVAEKHV
 230 PKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGN
 290 LVYRFCD---VKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKII----GIFSGH
 the food-
 171 LTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHV
 Gaps
 PubMed=15115801; DOI=10.1093/nar/gkh562;
Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
Porberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.,
"Whole genome comparisons of serotype 4b and 1/2a strains of the food
borne pathogen Listeria monocytogenes reveal new insights into the
 64;
 Length 316;
 9.1%; Score 194; DB 2; Length 316
24.0%; Pred. No. 5.2e-08;
Live 43; Mismatches 143; Indels
 Listeria monocytogenes (serotype 4b / strain F2365).
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
 PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN 1.
Complete protecome; Hydrollaes; Protease; Serine protease.
SEQUENCE 450 AA; 48793 WW; 54C79A67510FAD4A CRC64;
 core genome components of this species.";
Nucleic Acids Res. 32:236-2395(2004).
EMBL. AE017328, AATO4659.1;
EMBL. AE017328, AATO4659.1;
EMBL. AE017328, EILTYPSIN activity, IEA.
GO; GO:0006295; F:LTYPSIN activity, IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001256; Peptidase S1B.
InterPro; IPR001259; Peptidase S1B.
InterPro; IPR001903, Pept_Ser_Gys.
Pfam; PF07158; ChW; 3.
PRINTS; PR00839; VBPROTEASE.
316 AA; 33611 MW; 96D7552CB7089B09 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 450 AA
 : | : : | 112 | 1292 -----SSYNRGTRITKEVFDNLTNW 311
 344 QWVDMNGSPQDFNVAVRITPLKYAQICYW 372
 PRT;
 1900;
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273 PGGRIHFSGYDNDRP-GNLVYRFCDVKDETYDLLYQQ--CDAQPGASGSGVYVRMWKRQQ 329
 272 GDFTANLVGYPGDKPMGTMWKASCEVHAENIAPEYFQYDCDTFPGSSGSSVYAYDTKSKQ 331
 106 --FGWQWAKQWHVNPPYRRRPSGL------HDVGLIELERPFSPSPGHFQLWSPN 152
 153 RODLERLRNTRLLHISGYPADKPDGTQWEHSERLDRITERQLFYSVDTCPGHSGAPV--- 209
 169 YGSCSATLIGPRTVLTAAHCLYSHEDKDWL--SEYLFV-------PGLNGSTA--- 212
 270 KQ----LPGGR-IHFSGYDNDRPGNLVYRFCDVKDE-TYDLLYQQCDAQPGASGSGVYVR 323
 213 DDAPFGAFTYESAYVLQGFIDNYQGYYGSVIPWDLGIITLKQDVGTNLGWLGYA-NYDDL
 STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
 158 TGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGF-LKPKFKDGGRGANDSTSAMPEQ
 217 MKFQWIRVKRTHV-----PKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPA
 EQMKFQWIRVKRTHVPKGWIKGNANDIG--MDYDYALLELKKPHKRKFMKIGVSPPAKQL
 Gaps
 52;
 332 R------IITG---VNVAESP-DANTAVRLN----AANVQWINSLY 363
 330 QKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNY 377
 ch 7.4%; Score 158; DB 2; Length 271; I Similarity 29.0%; Pred. No. 4.8e-05; 67; Conservative 22; Mismatches 90; Indels 5
 Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium.
 PEAM, PF00089; Trypain; I.
PRINTS; PR00722; CHYMCTRYPSIN.
PRINTS; PR00839; VBPRCTEASE.
SMART; SM00030; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS01134; TRYPSIN DIM; UKNOWN 1.
COMDIACE DICTOCOME; HYDROIN HIS; UNKNOWN 1.
COMDIACE 271 AA; 30385 MW; 37659307C63D0D9C CRC64;
 -i- SIMILARITY: Belongs to peptidase family S1.

EMBL, AP003010; BAB53084.1, -
GO, GO:0004263; F:CHYMOLTYPRIN activity; IEA.
GO; GO:0004295; F:LTYPSIN activity; IEA.
GO; GO:0006508; P:Proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001256; Peptidase S1A.
InterPro; IPR001256; Peptidase S1A.
InterPro; IPR009206; Peptidase S1A.
InterPro; IPR0090316; Peptidase S1A.
InterPro; IPR0090031; Pept Ser_Gys.
 Last sequence update)
Last annotation update)
 271
 Glutamic acid specific endopeptidase
 Created)
 OrderedLocusNames=m116878;
Rhizobium loti (Mesorhizobium loti)
 (TrEMBLrel. 26,
 PRELIMINARY;
 DNA Res. 7:331-338(2000)
 (TrEMBLrel.
 SEQUENCE FROM N.A.
 NCBI_TaxID=381;
 01-OCT-2001
01-OCT-2001
 Query Match
 Local
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 Matches
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 13;
 158
 214
 128 RQIYGYDSRFSIFGKDFLLN---YPFSTS----VKLSTGCT----GTLVAEKHVLTAAHC 176
 KTIFGGD-----GRKLVTŇTTQYPYSTSAYLVMEFPNGKTYIGSGQLIGEDSVLTAAHC 146
 177 IHDGKTYVVKGTQKLRVGFLKPKFKDGG-----RGANDSTSAMPEQMKFQWIRVKRTH 228
 229 VPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKOLPGGRIHFSGYDNDRPG 288
 182 VPKEWTKKEPS----TEDYGVIKLDKNIGTKTGTMGLTTNT----SGAITISGYHGDKKG 233
 289 NLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDM 348
 234 KLYTQTGNISQVTANNVFYRLDTTGGSSGSGVY-----NSKKQILAV-NAYEYLNG 283
 112 ANGADGAERKTEDPGLGEGEAGRQVFGPDDREQVRNTK---TYPFSAIGYLEAKSAKTGS 168
 147 LY-GK-----KDGGWAKKVTVYPGYNGT-----KAPFGTAKARKMY 181
 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Marsuno A., Matsuno A., Matsuno A., Takeuchi Y., Yamada M., Tabata K., Shimpo S., Sugimoto M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 SSSGDGAQHR-DSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFST-----SVKLST
 --GCTGTLVAEKHVLTAAHCI--HDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMP
 Gaps
 72;
 53;
 DB 2; Length 364;
 8.8%; Score 188; DB 2; Length 450; 25.9%; Pred. No. 2.6e-07; tive 43; Mismatches 85; Indels
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
 Pfam, PF00089; Trypein; 1.
PRINTS; PR00839; VBPROTEASE.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Complete proteome; Hydrolage; Protease; Serine protease.
SEQUENCE 364 AA; 39034 MW; 13BE653270E7CDD3 CRC64;
 Indels
 GO: GO: 0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR001254; Peptidase_SI. InterPro; IPR008256; Peptidase_SIB. InterPro; IPR009003; Pept_Ser_Cys.
 Last sequence update)
Last annotation update)
 Mismatches 114;
 8.4%; Score 178.5; DB 2 27.1%; Pred. No. 1.3e-06;
 349 NGSPODFNVAVRITPLKYAQICYWIKGNYL 378
 284 TGD----NFGTRITKEKLNNIYTWAFDNNL 309
 364 AA.
 EMBL; AP003001; BAB50229.1; -. GO:0004295; F:trypsin activity; IEA
 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last sequ
Glutamyl endopeptidase (EC 3.4.21.19)
OrderedLocusNames=ml13306;
 Rhizobium loti (Mesorhizobium loti)
 MEDLINE=21082930; PubMed=11214968;
 43;
Query Match
Best Local Similarity 25.9*
 DNA Res. 7:331-338(2000).
 Conservative
 PRELIMINARY;
 Mesorhizobium loti."
 Similarity
 STRAIN=MAFF303099;
 SEQUENCE FROM N.A
 NCBI_TaxID=381;
 Query Match
Best Local Simi
Matches 78;
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This invention describes novel human transmembrane containing proteins that their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from nutritional uses, cytokine and cell differentiation, immune stimulation/suppression, haematopoiesis regulatory, tissue growth, activin/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic, receptor/linhibin, tumour inhibitor, anti-inflammatory and other undefined activities. The cDNAs can be utilized as probes for gene diagnosis and as gene sources for gene therapy. The cDNAs can also be used for large scale
 Disclosure; Page 87-89; 89pp; English.
 AAY08660;
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 1 MAGIPGLLFLLFFLLCAVGQ......LKYAQICYWIKGNYLDCREG 383
 July 1, 2005, 20:52:53 ; Search time 98.1294 Seconds
 Aay08657 Aay13390
 Aay87270 B
Aay53627 B
Aab25618 B
 Aab25592 B
Adc78573 B
Aab80258 B
Aab48974 B
 Aau29048 Abu58424 Abu71636 Abu84287 Abu84287 Abr66161 Abr65551 Abu89391 Abu89851 Abu898851 Abu71491 Abu71491
 Abr68100 H
Abu96153 N
Abu92584 H
 Aay88277
 2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 seqs, 386760381 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 ADC78573
AAB80258
 ABR68100
ABU96153
ABU92584
 AAY87270
 AAB25618
 ABU71636
 4BU84287
 AAY88277
 AAY53627
 AAB48974
 ABU58424
 ABU87972
 ABR66161
 ABR65551
 ABU71491
 Gapop 10.0 , Gapext 0.5
 geneseqp2003as:*
geneseqp2003bs:*
 A_Geneseq_16Dec04:*
 geneseqp1980s:*
geneseqp1990s:*
 geneseqp2002s:*
 geneseqp2000s:*
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 geneseqp20048:*
 length: 0
length: 2000000000
 US-09-658-677-18
2080
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|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|--|
| Human    | Human    | Human    | Human    | Human    | Novel    | Novel    | Novel    | Human    | Human    | Human    | Human    | Human    | Novel    | Human    | Human    | Human    | Human    | Human    | Human    |  |
| Abo08661 | Abo02713 | Abr74867 | Abr94629 | Abu85602 | Abu98762 | Abu97977 | Abu91683 | Abu71937 | Abu89376 | Abu86217 | Abu67430 | Abu80458 | Abo01820 | Abr99376 | Abr98766 | Abo16289 | Abr92189 | Abo18830 | Abr78251 |  |
|          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |  |
| AB008661 | ABO02713 | ABR74867 | ABR94629 | ABU85602 | ABU98762 | ABU97977 | ABU91683 | ABU71937 | ABU89376 | ABU86217 | ABU67430 | ABU80458 | ABC01820 | ABR99376 | ABR98766 | AB016289 | ABR92189 | ABO18830 | ABR78251 |  |
| 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        | 9        |  |
| 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      | 383      |  |
| 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    |  |
| 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     | 2080     |  |
| 56       | 27       | 28       | 53       | 30       | 31       | 32       | 33       | 34       | 35       | 36       | 37       | 38       | 39       | 40       | 41       | 42       | 43       | 44       | 45       |  |
|          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |  |

## ALIGNMENTS

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Transmembrane domain; human; nutrition; cytokine; cell differentiation; immune estimulatedion; immune estimulation; haemacopoiseis; activin; regulatory tissue growth; inhibin; chemostatic; chemokinetic; haemostatic; thrombolytic; tumour inhibitor; anti-inflammatory;
 Novel proteins containing transmembrane domains, useful as anti-
inflammatories, immune stimulators/suppressors and tissue growth
AAY08660 standard; protein; 383 AA
 97JP-00323129.
 98WO-JP005238
 SAGA) SAGAMI CHEM RES CENT.
 Kato S, Kimura T, Sekine
 (first entry)
 gene therapy; screening
 PROT-) PROTEGENE INC.
 WPI; 1999-357835/30
 WO9927094 Seg ID 12
 WO9927094-A2.
 20-NOV-1998;
 25-NOV-1997;
 09-AUG-1999
 Homo sapiens
 03-JUN-1999.
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Sequence 383 AA;
 Homo sapiens
 25-JUN-1999
 181
 301
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 Query Match
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 TYDLLYQQCDAQPGASGSGVYVRMMKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
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expression of proteins. The transformed cells can be used for detection of the corresponding ligands and for screening of novel low-molecular pharmaceuticals
 Transmembrane domain; human; nutrition; cytokine; cell differentiation; immune etimulation; haematopoleals; activin; regulatory tissue growth; inhibin; chemostatic; chemokinetic; haemostatic; thrombolytic; tumour inhibin; anti-inflammatory;
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 VSSSCGPOCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 Gaps
 Human transmembrane domain containing protein from clone HP10493
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 Length 383;
 Indels
 100.0%; Score 2080; DB 2; 100.0%; Pred. No. 1.8e-145;
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 0; Mismatches
 ITPLKYAQICYWIKGNYLDCREG 383
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 383
 Kimura T, Sekine S;
 98WO-JP005238
 CHEM RES CENT.
 97JP-00323129
 protein;
 WPI; 1999-357835/30.
N-PSDB; AAX77690, AAX77691.
 (first entry)
 Best Local Similarity 100.
Matches 383; Conservative
 screening
 AAY08657 standard;
 (SAGA) SAGAMI CHE (PROT-) PROTEGENE
 Sequence 383 AA;
 therapy;
 20-NOV-1998;
 25-NOV-1997;
 Homo sapiens
 WO9927094-A2
 09-AUG-1999
 AAY08657;
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This invention describes novel human transmembrane containing proteins and their encoding nucleic acids. Although no specific use is given for the proteins, they may have a range of activities selected from nutritional uses, cytokine and cell differentiation, immune stimulation/suppression, haematopoiesis regulatory, tissue growth, activila/inhibin, chemostatic/chemokinetic, haemostatic/thrombolytic, receptor/lighand, tumour inhibitor, anti-inflammatory and other undefined activities. The CDNAs can be utilized as probes for gene diagnosis and as gene sources for gene therapy. The connected for large scale expression of proteins. The transformed cells can be used for large scale expression of proteins. The transformed cells can be used for detection of the corresponding ligands and for screening of novel low-molecular
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 Zollinger-Ellison syndrome; gastrointeetinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzhelmer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLINYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKI IGIFSGHQWVDMNGSPQDFNVAVR
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 1 MAGIPGLIFFLEFELCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 Gaps
Novel proteins containing transmembrane domains, useful as anti-
inflammatories, immune stimulators/suppressors and tissue growth
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0
 Secreted protein; transmembrane protein; human; enterocolitis;
 100.0%; Score 2080; DB 2; Length 383; 100.0%; Pred. No. 1.8e-145; ive 0; Mismatches 0; Indels 0
 Amino acid sequence of protein PRO307
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Claim 1; Page 68-69; 89pp; English.
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 AAY13390 standard; protein; 383
 (first entry)
 Best Local Similarity 100.
Matches 383; Conservative
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cc encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PR0211 and PR0217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, c. Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells can cancer. PR0265 can be used as for fibromodulin, e.g. for reducing dermal cancer. PR0265 can be used as for fibromodulin, e.g. for reducing dermal cancer. PR0265 can be used as a target for anti-tumor drugs. PR0533 may be used in the treatment of Ugher Syndrome or Atrophia areates; PR0530 can be used as an anti-thrombotic agent; PR0287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PR0317 can be used for treating problems of the kidney, uterus, endometrium, c.g. blood vessels, or related tissue, e.g. in the heart of genital tract
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
 241 IGMDYDALLELKKPHKRKEMKIGVSPPAKQLPGGRIHPSGYDNDRPGNLVYRFCDVKDE 300
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 KTYVKGTQKLRVGFLKPKEKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185;
TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine;
secreted protein; transmembrane protein; gene therapy; vaccine;
 0; Сарв
 Length 383;
 0; Indels
 100.0%; Score 2080; DB 2;
100.0%; Pred. No. 1.8e-145;
iive 0; Mismatches 0;
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
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 AAY88277 standard; protein; 383
 diagnosis; treatment; detection
 16-OCT-2000 (first entry)
 Matches 383; Conservative
 Human TANGO 186 protein.
 Local Similarity
 Sequence 383 AA;
 WO200018904-A2
 Homo sapiens.
 06-APR-2000
 241
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 Query Match
Best Local &
 AAY88277
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 AAY13344-403 represent secreted and transmembrane human proteins. The CDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration.
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 Chen
 Pennica D,
 Goddard A,
 Claim 12; Fig 96; 320pp; English
 9705-0059119P

9705-0059121P

9705-0059124P

9705-0059263P

9705-0059268P

9705-00629184P

9705-00629184P

9705-00629148P

9705-00629148P

9705-0063121P

9705-0064218P

9705-0064218P

9705-0064218P

9705-0064218P

9705-0064218P

9705-006421P

9705-006631P

9705-006631P

9705-006631P
 97US-0059113P.
97US-0059115P.
97US-0059117P.
 (GETH) GENENTECH INC.
 Wood WI, Gurney AL,
 WPI; 1999-229533/19.
 N-PSDB; AAX52261
 WO9914328-A2
 17-SEP-1997;
17-SEP-1997;
 1997
 25-MAR-1999
 2-NOV-1
 OCT-1
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This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The caids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may also be used to detect and quantify the presence of TANGO mucleic acids in a sample and therefore identify or diagnose diseases associated with inappropriate TANGO expression (e.g. diseases related to over or under expression of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a pastients own production of the polypeptide of to rectify mutations that parties own production of an abnormally active polypeptides and cancagonists of TANGO expression and activity which may be used to identify and producing antibodies to rectify mutations that antiganists of TANGO expression and activity which may be used for inhibiting the activity of TANGO proteins which may be used for inhibiting the presence of TANGO proteins which may be used for inhibiting the activity of TANGO proteins in samples and therefore identify patients in whom the protein is sover- or under-expressed. This sequence represents the human TANGO 186 protein described in the method of the invention
 Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression.
 Length 383;
 (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 Claim 9; Fig 13; 249pp; English.
 99WO-US022817.
 98US-00164220
 98US-00164169
 N-PSDB; AAA39945, AAA39946.
 WPI; 2000-293144/25
 Sequence 383 AA;
 30-SEP-1999;
 30-SEP-1998;
 02-OCT-1998;
 Barnes TM;
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100.0%; Score 2080; DB 3; 100.0%; Pred. No. 1.8e-145; Live 0; Mismatches 0; Query Match Best Local Similarity 100.' Matches 383; Conservative 8

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 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPPSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
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 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 VSSSCGPQCHKGTPLPTYBEAKQYLSYBTLYANGSRTBTQVGIYILSSSGDGAQHRDSGS
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
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RESULT 5 4AY87270

AAY87270 standard; protein; 383 AA

AAY87270;

11-MAY-2000 (first entry)

Human signal peptide containing protein HSPP-47 SEQ ID NO:47.

Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn; disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect; muscular dystrophy

Ното варіепв.

WO200000610-A2

06-JAN-2000.

99WO-US014484. 25-JUN-1999;

98US-0090762P :6-JUN-1998;

98US-0102686P. 98US-0112129P. 31-JUL-1998; 01-OCT-1998; 11-DEC-1998;

(INCY-) INCYTE PHARM INC.

YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR; Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL; Akerblom IE, Tang Bandman O; Lal P,

WPI; 2000-160673/14.

N-PSDB; AAZ98155.

New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardlovascular disease.

Claim 1; Page 192-193; 327pp; English.

human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anti-inflammatory, antimicrobial, nootropic, hepatotropic, carticovascular and antiasthmatic activities, and can be anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, carthma, crohn's disease, Alzhenimer's Parkinson's or Huntington's cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, carthma, crohn's disease, Alzhenimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for detecting HSPP in standard hybridisation and amplification assays (for disponsis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise 

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361 ITPLKYAQICYWIKGNYLDCREG 383
 N-PSDB; AAZ36233
 Sequence 383 AA;
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 24-SEP-1998;
30-SEP-1998;
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specific antibodies (Ab) and to screen for agonists and antagonists (Detential therapeutic agents). Ab are used to diagnose, or monitor, HSPP -related diseases (in usual immunosasys), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural
 120
 120
 180
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
 240
 240
 300
 241 IGMDYDYALLELKKPHKRKFWKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 360
 301 TYDLLYQQCDAQPGASGSGVYVRWWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 9
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 1 MAGIPGLEPLEFELCAVGOVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 1 MAGIPGLLFFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 SGKSRRKRQIYGYDSRFSIFGKDFLLMYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 Bone marrow secreted protein; bone marrow stromal cell; cytokine; cell proliferation; cell differentiation; hematopoiesis; anaemia; myeloid cell deficiency; lymphoid cell deficiency; myeloid cell; earthroid progenitor colony stimulating factor; granulocyte; monocyte; macrophage; myelo-suppression; megakaryocyte; platelet disorder; thrombocytopenia; hematopoeitic stem cell; stem cell disorder; aplastic anaemia; bone differentiation; paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon; ligament; nerve; wound healing; tissue repair; burn; incision; ulcer; bone fracture; cartilage damage; artificial joint.
 0; Gaps
 100.0%; Score 2080; DB 3; Length 383; 100.0%; Pred. No. 1.8e-145; ive 0; Mismatches 0; Indels 0
 A bone marrow secreted protein designated BMS192
 1. .19
/note= "signal peptide"
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Location/Qualifiers
 AAY53627 standard; protein; 383 AA
 98WO-US027008
 Query Match
Best Local Similarity 100.0
Matches 383; Conservative
 22-FEB-2000 (first entry)
 Sequence 383 AA;
 Homo sapiens.
 18-DEC-1998;
 W09933979-A2
 121
 181
 181
 241
 301
 Bources
 Peptide
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AAY53622-43 represent bone marrow secreted proteins of human bone marrow stromal cells. The proteins can exhibit cytokine, cell proliferation, or cell differentiation activity (either inducing or inhibiting). They can be used to support colony forming cells or factor-dependent cell lines, to regulate hematopoiesis, and to treat myeloid or lymphoid cell and cellideration of erythroid progenitor cells, and to treat various anaemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo. They can be used to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and coliferation of hematopoeitic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and triangles repair and replacement, and in the treatment of plump.
 and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints
 120
 120
 180
 180
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 9
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 181 KTYVKGTOKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 1 MAGIPGLIFILFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKOLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 1GMDYDYALLELKKPHKRKFMK1GVSPPAKQLPGGR1HFSGYDNDRPGNLVYRFCDVKDE
 Gaps
 New isolated human polynucleotide and secreted proteins can induce production of other cytokines in certain cell populations.
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 100.0%; Score 2080; DB 3; Length 383; 100.0%; Pred. No. 1.8e-145; ive 0; Mismatches 0; Indels 0.
 ;
0
 Claim 2; Page 81-82; 120pp; English.
97US-0068958P.
98US-0101603P.
98US-0102540P.
 Matches 383, Conservative
 2000-038344/03
 Best Local Similarity
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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606A80623 encode the 12 secreted protein sequences given in AAA80606A80623 encode the 12 secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antianteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antagonists may be used to treat prevent and/or diagnose various disease, discorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory powel disease, cronary disorders e.g. inflammatory bowel disease, cronary disorders e.g. inflammatory bowel disease, cronary arteriosclerosis and mycoarders; and also be used in wound healing and polynucleotide sequences may also be used in wound healing and polynucleotide sequences may also be used in wound healing and protein sequences may also be used in wound healing and protein gene #10 and protein gene #10 and protein gene #10 and protein gene #10 is located on chromosome 12.

Sequences AAB25616 E25618 represent genes which are related to the
 Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer,
 immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohr s disease; nepritits; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human; chromosome 12.
 antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal;
 Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic
 Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA,
 Protein encoded by human secreted protein gene #10
 Disclosure; Page 169; 803pp; English.
AAB25618 standard; protein; 383 AA
 wounds, and infectious diseases.
 99WO-US025031.
 98US-0105971P.
 GENOME SCI INC
 21-NOV-2000 (first entry)
 protein gene#10
 WPI; 2000-387742/33
 WO200029435-A1.
 (HUMA-) HUMAN
 Homo sapiens
 27-OCT-1999;
 28-OCT-1998;
 25-MAY-2000
 Greene JM;
 361
 secreted
 Ni G,
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Sequence 383 AA;

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 120
 120
 180
 180
 240
 240
 solated nucleic acid molecules encoding human secreted proteins are used
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 9
 immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disease, nephritis; hyperpoliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myccarditis; cancer; melanoma; lymphoma; wound healing; human; chromosome 12.
 Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal;
 1 MAGIPGELFLEFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 VSSSCGPQCHKGTPLPTYBEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 Gaps
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 Wei
 Protein encoded by human secreted protein gene #10 clone HUSQ05.
 ö
 Length 383;
 PA,
 Moore
 Indels
 Kenny JJ,
 Score 2080; DB 3;
Pred. No. 1.8e-145;
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 Mismatches
 Ruben SM, Olsen HS, Young PE, JM_i
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 AAB25592 standard; protein; 383 AA
100.0%; Sco
100.0%; Pre
 99WO-US025031
 98US-0105971P
 HUMA-) HUMAN GENOME SCI INC
 21-NOV-2000 (first entry)
 Conservative
 WPI; 2000-387742/33.
 Similarity
 WO200029435-A1
 Homo sapiens
 27-OCT-1999;
 28-OCT-1998;
 25-MAY-2000.
 Matches 383;
 301
 AAB25592;
 Query Match
 Local
 Greene
 RESULT 8
 AAB25592
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nucleotide sequences encoding them. The polymucleotide sequences given in MA80666-A80623 encode the 12 secreted protein sequences given in AA82566-B25593. The human secreted proteins sequences given in activities of the proteins include: immunosuppressant; anti-inflammatory; antiathritic; antirhemmatic, dermatological; antiporliferative; and antifungal activity. The proteins, polypeptides, agonists and intagence; antagonists and sease, claromists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple claromatory disorders e.g. inflammatory bowel disease, cronary paraproteinaemias and purpura; cardovascular disorders such as paraproteinaemias and purpura; cardovascular disorders e.g. coronary arteriosclerosis and mycoarditis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and protein sequences are represented in sequences AAA80615 and AAB25616-B25618 represent alternative secreted protein gene #10 is located on chromosome 12.
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
 120
 240
 240
 300
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 360
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
 9
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 antiinflamatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVG1Y1LSSSGDGAQHRDSGS
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 1 MAGIPGLIFILLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 Gaps
 ö
 100.0%; Score 2080; DB 3; Length 383; 100.0%; Pred. No. 1.8e-145; tive 0; Mismatches 0; Indels 0.
 to 12 secreted human
 Claim 1; Page 684-685; 803pp; English.
 Ź
 ITPLKYAQICYWIKGNYLDCREG
 ADC78573 standard; protein; 383
 present invention relates
 01-JAN-2004 (first entry)
 Query Match
Best Local Similarity 100.
Matches 383; Conservative
 secreted protein gene#10
 Human PRO307 protein.
 Sequence 383 AA;
 121
 181
 241
 361
 ADC78573;
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 The invention relates to a novel nucleic acid encoding a PRO polypeptide. The polypeptides and polynuclectides of the invention may be useful as research tools and as therapeutics for treating enterocolitis. Zollinger-Blison syndrome, gastrointestinal ulceration, psoriasis, cancer, Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal scarring and wound healing, nerve repair, thrombosis, bone and/or cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple infertility, premature aging, AIDS, diabetes complications and stroke. The molecules may also be utilised during gene therapy procedures and transgenic animal production. The current sequence is that of the human
 Novel nucleic acids encoding secreted and transmembrane polypeptides with homology, e.g. to growth and cancer-associated antigens.
 120
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 neurotrophic, osteopathic, antiasthmatic, antiarthritic, antirheumatic, antiarteriosclerotic, cardiant, antidiabetic, cerebroprotective, thrombolytic, immunomodulator, enterocolitis, Zollinger-Ellison syndrome,
 gastrointeerinal ulceration; psoriasis; cancer; Parkinson's disease; Alzheimer's; ALS; neuropathy; dermal scarring; wound healing; areve repair; thrombosis; bone; cartilage formation; angiogenesis; asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder; atherosclerosis; cardiac injury; infertility; premature aging; AIDS; diabetes; stroke; gene therapy; transgenic; PRO; human.
 9
 1 MAGIPGLEFLLEFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 SGKSRRKROIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 Gaps
 neuroprotective; vasotropic; chemotaxic; angiogenic;
 ;
0
 Length 383;
 Wood
 Indele
 Pennica D,
 100.0%; Score 2080; DB 3;
100.0%; Pred. No. 1.8e-145;
ive 0; Mismatches 0;
 Gurney AL, Hillan K,
 Claim 12; SEQ ID NO 261; 355pp; English.
 99WO-US021090.
 PRO protein of the invention.
 98WO-US019330
 383; Conservative
 (GETH) GENENTECH INC.
 Goddard A,
 WPI; 2000-271434/23.
 Query Match
Best Local Similarity
 N-PSDB; ADC78572.
 Sequence 383 AA;
 WO200015796-A2.
 Homo sapiens.
 15-SEP-1999;
 16-SEP-1998;
 23-MAR-2000
 nootropic;
 121
 Chen J,
Yuan J;
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Matches
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us-09-658-677-18.rag

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diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, inchaemias such as coronary ischaemia, atherosoleroais), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and
 Sequence 383 AA;
 gene mapping
 Homo sapiens
 04-MAY-1998;
 24-APR-1997;
17-APR-1998;
 27-MAR-2001
 US6153420-A.
 28-NOV-2000
 61
 361
 121
 181
 301
 301
 AAB48974;
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 Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 TYDLLYQQCDAQPGASGSGVYVXMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 Human, PRO, dermatological, antipsoriatic, cytostatic, antiinflammatory, antiparkinsonian nootropic; neuroprotective; vulnerary, cardiant, antiangiogenic, vasotropic; antiasthmatic; antirheumatic, cancer; antiarthritic; antiinfertility; antidabetic; antiviral; diabetes; ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 Hillan KJ, Kljavin IJ;
Stewart TA, Tumas D;
 Ferrara N;
 Eaton DL,
 Ashkenazi AJ, Botstein D, Desnoyers L,
Filvaroff E, Fong S, Gao W, Gerber H,
 Fong S, Gao W, Gerber H, Grimaldi CU, Gurney AL, Pan J, Paoni NF, Roy MA, Mood WI;
 383
 Ş
 ITPLKYAQICYWIKGNYLDCREG
 AAB80258 standard; protein; 383
 Claim 1; Fig 96; 393pp; English.
 99WO-US028214.
99WO-US028313.
99WO-US028564.
99WO-US028565.
 99US-0143048P.
99US-0145698P.
99US-0146222P.
99WO-US020594.
 99WO-US021090.
99WO-US021547.
99WO-US023089.
 99WO-US030095.
99WO-US030911.
99WO-US030999.
 2000WO-US004414
 2000WO-US000219
 (first entry)
 ischaemia; inflammation
 (GETH) GENENTECH INC.
 Human PRO307 protein.
 WPI; 2001-081051/09.
 N-PSDB; AAF72419
 WO200104311-A1
 Mather JP, P
Williams PM,
 Homo sapiens
 22-FEB-2000;
 13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
 05-OCT-1999;
29-NOV-1999;
30-NOV-1999;
02-DEC-1999;
 02-DEC-1999;
16-DEC-1999;
20-DEC-1999;
 05-JAN-2000;
 Godowski PJ,
 24-APR-2001
 08-SEP-1999
 20-DEC-1999
 18-JAN-2001
 301
 361
 361
 AAB80258;
 301
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 RESULT 10
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 240
 120
 120
 180
 240
 300
 180
 360
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 9
 9
 Human Zsigll; serine protease; chromosome 11q22.1; elastase homologue; glutamyl endopeptidase homologue; factor X homologue; trypsinope; trypsinope; trypsinope; protease homologue; protease homologue; collagenase homologue; protein degradation; food processing; brewing; alcohol production; laundry detergent component.
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 1 MAGIPGLIFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 Gaps
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Length 383;
 0; Indels
Query Match 100.0%; Score 2080; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-145; Matches 383; Conservative 0; Mismatches 0;
 Human Zsigl3 variant #3, SEQ ID NO:18.
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Z
 AAB48974 standard; protein; 383
 98US-00072384
 97US-0044185P.
 (first entry)
 (ZYMO) ZYMOGENETICS INC.
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The invention relates to human Zsigl3 proteins (AAB48972-B48974), and to DNA encoding them (AAG9182-C91784). The invention also relates to expression vectors and host cells comprising a human Zsigl3 DNA, and the recombinant production of a human Zsigl3 protein or its precursor. Zsigl3 is a serine protease, and has significant homology to Bacillus licheniformis glutamyl endopeptidase, human clotting factor X, human elastase, rat mast call protease, Streptomyces griseus trypsin, bovine trypsinogen, and Hypoderma lineatum collagenase. The gene encoding human Zsigl3 is located on chromosome 1122:1. Zsigl3 is useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing compositions. It may also be used in industrial applications in which proteases are utilised, including food processing, brewing and alcohol production, and as a component of a laundry detergent. The present sequence represents a human Zsigl3 variant
 ö
 300
 120
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
 240
 120
 SGKSRRKRQ1YGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
 240
 300
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 360
 9
 9
 New isolated serine protease (designated Zsigl3), useful in industrial processes to degrade unwanted proteins or alter the characteristics of protein-containing composition, as well as in industrial applications
 301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQXWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 61 VSSSCGPQCHKGTPLPTYBEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 Gaps
 PRO polypeptide, mammal; tumour; cancer; human; cattle; horse; sheep;
 °,
 100.0%; Score 2080; DB 4; Length 383; 100.0%; Pred. No. 1.8e-145;
 0; Indels
 0; Mismatches
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Š
 Human PRO polypeptide sequence #25.
 Claim 1; Col 41-44; 26pp; English
 ITPLKYAQICYWIKGNYLDCREG
 AAU29048 standard; protein; 383
 (first entry)
 Best Local Similarity 100.
Matches 383; Conservative
 WPI; 2001-060090/07.
N-PSDB; AAC91784.
 Sequence 383 AA;
 (e.g. brewing)
Sheppard PO;
 18-DEC-2001
 61
 301
 361
 121
 181
 AAU29048;
 Query Match
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 AAU29048
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dog, cat; pig; goat, rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
 The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 Gurney AL;
 Godowski PJ,
 A, Go
Zhang
 L, Goddard
Wood WI,
 Claim 11; Fig 50; 774pp; English
 2000WO-US008439.
2000US-01946479
2000US-01946479
2000US-0196000P.
2000US-0196000P.
2000US-0196187P.
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2000US-0196187P.
2000US-0196187P.
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2000US-0198187P.
 Baker KP, Chen J, Desnoyers
Pan J, Smith V, Watanabe CK,
 2000US-0186968P.
2000US-0189320P.
2000US-0189328P.
 2000US-0190828P.
2000US-0191007P.
2000US-0191048P.
 2000US-0191314P.
2000US-0192655P.
 2000WO-US014042.
 2000US-00644848.
2000WO-US023328.
 2000WO-US005841
2000US-0187202P
 2000WO-US006884
 2000US-0193032P
 2000US-0193053P
 2000WO-US013705
 2000WO-US014941
 2000WO-US015264
 2000US-0209832P
 (GETH) GENENTECH INC.
 WPI; 2001-602746/68.
N-PSDB; AAS45949.
 Chen J,
 02-MAR-2000;
03-MAR-2000;
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14-MAR-2000;
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 180
 240
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 360
 360
and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation of differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nuclaic acids can be used for genetic analysis of individuals with genetic disorders
 9
 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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 Human, PRO, cytostatic, tumour, cancer, breast, lung, stomach, liver,
dog, cat, cow, horse, sheep, pig, goat, rabbit, ADEPT,
antibody-dependent enzyme mediated prodrug therapy.
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 97US-0059263P.
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97US-0062250P.
97US-0063486P.
97US-0063120P.
 2002US-00176492
 (first entry)
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 Sequence 383 AA;
 US2003027272-A1
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 21-JUN-2002;
 18-SEP-1997;
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TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
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 Human; PRO; secreted polypeptide; transmembrane polypeptide;
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Best Local Similarity 100.0%; Pred. No. 1.8e-145;
Matches 383; Conservative 0; Mismatches 0;
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98US-010251P.
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98US-0102540P.
98US-0102570P.
98US-0102570P.
98US-0102570P.
98US-0102584P.
98US-0102570P.
 16-JUN-2003 (first entry)
 Human PRO polypeptide #47.
17-SEP-1998, 17-SEP-1998, 18-SEP-1998, 18-SEP-1998, 23-SEP-1998, 23-SEP-1998, 23-SEP-1998, 24-SEP-1998, 29-SEP-1998, 29-SEP-1998, 29-SEP-1998, 30-SEP-1998, 30-SE
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 ABU71636;
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 301
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26-AUG-1998;
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Gaps

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Indels

Length 383;

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pathological disorder; cardiac insufficiency disorder; protein secretion;
 pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis; skin disease; Keratinocyte differentiation; epithelial cancer; tumour; lung squamous cell carcinoma; epidermoid carcinoma; yulva; glioma; cytostatic; cardiant; endocrine; antidiabetic; gastrointestinal; antiulcer; dermatological; vulnerary.
 9705-0059113P

9705-0059113P

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9705-0053124P

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9705-0055314P
 98WO-US019330
 99WO-US021090
99WO-US021547
 2001US-00909088
 98WO-US019177
 98WO-US019437
 98WO-US025108
 99WO-US020944
 US2002146709-A1
 Homo sapiens
 18-JUL-2001;
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 .6-SEP-1998
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The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polynucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and tumours, in therapeutic treatment of asorders involving pathological secretion by the pancreas, including disbetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal casions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriases, epitholial cancers such as lung squamous cell carcinoma, epitholial carcinoma of the vulva and gliomas). The sequences can be used as molecular markers for protein celectrophoresis purposes and can be utilised in protein-protein binding assays, biochemical screening assays, immunoassays and cell-based assays. This sequence represents a human PRO polypeptide of the invention
 Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
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 Ferrara N;
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Kljavin IJ;
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 Botstein D, Desnoyers L, Eaton DL, Ferrara Fong S, Gao W, Gerber H, Gerritsen ME, Go Grimaldi JC, Gurney AL, Hillan KJ, Kljavin an J, Paoni NF, Roy MA, Stewart TA, Tumas Wood WI;
 Claim 12, Fig 96; 473pp; English.
 20-MAR-2000; 2000WO-US007377.
30-MAY-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
02-UUN-2000; 2000WO-US015264.
28-UUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US0203128.
18-SEP-2000; 2000US-00653328.
 99WO-US028301.
99WO-US028564.
99WO-US028565.
99WO-US030095.
 99WO-US030911
 11-FEB-2000; 2000WO-US003565
22-FEB-2000; 2000WO-US004414
24-FEB-2000; 2000WO-US005004
02-MAR-2000; 2000WO-US005841.
 99WO-US028214
99WO-US028313
 2000WO-US000219
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 WPI; 2003-328338/31.
N-PSDB; ACA59109.
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05-JAN-2000;
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120

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181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND

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 Human; secreted and transmembrane protein: PRO; gene therapy; tumour necrosis factor-alpha release; TNF-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour; adrenal tumour; rung tumour; cervical tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
 Novel human secreted and transmembrane protein PRO307
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 97US-0059263P.
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98US-0077649P.
 98US-0080327P.
98US-0080333P.
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 26-JUN-2002; 2002US-00183012
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| 59, Appl |            | 18-944-            | m | 241 |     | 115.5 | 41 |
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| ', Appli | Sequence 7 | US-09-387-375-7    | 4 | 284 | 5.8 | 120   | 37 |
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## ALIGNMENTS

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US-0-072-384-18

1S-69-072-384-18

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Patent No. 6153420

GENERAL INFORMATION:

APPLICANT: SIEDPARA, Paul O.

TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES

TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES

TITLE OF INVENTION: ADM MATERIALS AND METHODS FOR MAKING THEM NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZYMCGENETICS: 100

STREET: 1201 Eastlake Avenue East CITTY: Seattle Avenue East CITTY: Seattle Avenue East CITTY: Seattle EASTLE FORM:

COUNTRY: USA

ZIP: 98102

COMPUTER: INA Compatible OCHAPUTER: ISA COMPUTER: SIENCE OCHAPUTER: ISA COMPUTER: INFORMATION:

REPERENCE! COCKET VINNERR: 97-16C1

TELECHANDE PARA: GATY E

TELECHANDE PARA: 206-442-6673

TELECHANDE CHARACTERISTICS: ISA COMPUTER: INFORMATION COUNTRY: SIGNAL SEQUENCE

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 APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timochy A.
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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TITLE OF INVENTION: Screted and Transmembrane Polypeptides and Nucleic
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CURRENT PILING DATE: 2001-07-17
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR PAPLICATION NUMBER: US 60/143,048
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Patent No. 6635468
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Godowski, Paul J.
Grimaldi, Christopher J.
 APPLICANT: Genentech, Inc.
APPLICANT: AShkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Ererara, Napoleone
APPLICANT: Ferrara
 100.0%;
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 Conservative
 Pan, James
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APPLICANT:
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PRIOR FILING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: PCT/US99/21647
PRIOR FILING DATE: 1999-10-05
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 ORGANISM: Homo Sapien
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Wood, William, I.
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 Berritsen, Mary E
 aoni, Nicholas F.
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 Kljavin, Ivar J.
Mather, Jennie P.
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Genentech, Inc.
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Botstein, David
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 Goddard
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 APPLICANT: Williams, P. Mickey
APPLICANT: Wood William, I.
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Grimaldi, Christopher J.
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
 Gerber, Hanspeter
Gerritsen, Mary E
 Gurney, Austin L.
Hillan, Kenneth,
 Kljavin, Ivar J.
Mather, Jennie P.
 Matches 383; Conservative
 Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
Gao, Wei-Qiang
 umas, Daniel
 Filvaroff,
 Рап, Јашев
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 US-09-902-775A-261
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Pred. No. 5.4e-220;
 APPLICANI; WOOG, WILLIAM, 1.

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PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-11-39
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-12-06
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 Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Ferrara, Napoleone
Filvaroff, Ellen
 Timothy A
 Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
 TYPE: PRT
ORGANISM: Homo Sapien
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PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-06
PRIOR P
 APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09906700 Patent No. 6723535 GENERAL INFORMATION:
 ORGANISM: Homo Sapien
US-09-902-775A-261
 US-09-906-700-261
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 and Transmembrane Polypeptides and Nucleic
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ö
 APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-00-07
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PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
 Godowski, Paul J.
Grimaldi, Christopher J.
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 Length 383;
 Indels
 100.0%; Score 2080; DB 4;
100.0%; Pred. No. 5.4e-220;
tive 0; Mismatches 0;
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-16
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
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PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-0105
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 US-09-904-920A-261
; Sequence 261, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
 Query Match
Best Local Similarity 100.
Matches 383; Conservative
 ; ORGANISM: Homo Sapien
US-09-903-603A-261
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us-09-658-677-18.rai

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 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-26
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: APPLICANT: APPLICANT:
APPLICANT: Botstein, David
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Chang
Gerber, Hangpeter
Gerritsen, Mary E.
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Williams, P. Mickey Wood, William, I.
 Desnoyers, Luc
Eaton, Dan L.
 Goddard, A.
 Pan, James
 RESULT 8
US-09-909-064-261
 121
 APPLICANT:
APPLICANT:
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 APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2000-00-22
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
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PRIOR PLING DATE: 1999-09-15
 Query Match
100.0%; Score 2080; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.4e-220;
Matches 383; Conservative 0; Mismatches 0; Indels 0
 PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTHING
 PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-07
 Godowski, Paul J.
Grimaldi, Christopher J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
 Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Gerber, Hanspeter
Gerritsen, Mary E.
 Paoni, Nicholas F.
 Gurney, Austin L.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
 Wei-Qiang
 Goddard, A.
 Pan, James
 TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-920A-261
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Gaps ; 0

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and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Secreted and Transmembrane Prittle OF INVENTION: Secreted and Transmembrane Prittle OF INVENTION: Secreted and Transmembrane Prittle OF INVENTION: Acids Brooding the Same TITLE OF INVENTION: Acids Brooding the Same CURRENT APPLICATION NUMBER: US/09/905,381A CURRENT FILING DATE: 2001-07-13

PRIOR PELING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

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PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-08

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PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-11-30

PRIOR PELING DATE: 1999-11-00

PRIOR PELING DATE: 1999-12-00

 Godowski, Paul J.
Grimaldi, Christopher J.
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 Williams, P. Mickey Wood, William, I.
 Stewart, Timothy A. Tumas, Daniel
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 Paoni, Nicholas F.
Roy, Margaret Ann
 Gerritsen, Mary E
 Gerber, Hanspeter
 ilvaroff, Ellen
 Wei-Qiang
 ong, Sherman
 Goddard,
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT
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 Length 383;
 Indels
 0; DB 4;
5.4e-220;
 Query Match
100.0%; Score 2080;
Best Local Similarity 100.0%; Pred. No. 5.4
Matches 383; Conservative 0; Mismatches
 PRIOR PETLING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-20

PRIOR PLING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28665

PRIOR APPLICATION NUMBER: PCT/US99/30091

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-03

PRIOR PLING DATE: 1999-12-04

PRIOR PLING DATE: 1999-12-05

PRIOR PLING DATE: 1999-12-05

PRIOR PLING DATE: 1999-12-06

PRIOR PLING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

TYPER PRI PRIOR PLING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

TYPER PRI PRIOR PLING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

TYPER PRIOR PLING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

TYPER PRIOR PLING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

CRGANISM: HOMO Sapien

US-09-909-004-261
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
 361 ITPLKYAQICYWIKGNYLDCREG 383
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 RESULT 9
US-09-905-381A-261
 181
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| VIVIDER OF SEQ ID NOS: 423
| SEQ ID NO 261
| LENGTH: 383
| TYPE: PRT | TYPE: PRT | 100.0%; Score 2080; DB 4; Length 383; | Query Match | 100.0%; Score 2080; DB 4; Length 383; | Best Local Similarity 100.0%; Pred. No. 5.4e-220; | Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Sequence 261, Application US/09905381A Patent No. 6818746 GENERAL INFORMATION: APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi

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 Gaps
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 Sequence 15, Application US/09072384

Patent No. 6153420

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES
TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
 Length 383;
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 Query Match 100.0%; Score 2080; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.4e-220;
Matches 383; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944.
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO S: 423
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 ; ORGANISM: Homo Sapien
US-09-906-618-261
 RESULT 11
US-09-072-384-15
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 TYPE: PRT
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 240
 120
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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 Nucleic
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuclified of INVENTION: Secreted and Transmembrane Polypeptides and Nuclified OF INVENTION: Acids Encoding the Same FILE REFRENCE: 10466-14

FILE REFRENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,618

CURRENT FILING DATE: 2001-07-16

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26
 ITPLKYAQICYWIKGNYLDCREG 383
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 Sequence 261, Application US/09906618
Patent No. 6828146
PERERAL INPERMATION:
APPLICANT: Genentech, Inc.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 Ferrara, Napoleone
Filvaroff, Ellen
 Paoni, Nicholas F.
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
 361
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
 61
 181
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 APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
 361
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REFERENCE/DOCKET NUMBER: 97-16C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
 98.3%;
98.4%;
 NAME/KEY: Signal Sequence LOCATION: 1...19 OTHER INFORMATION: US-09-072-384-2
 E: Diskette
IBM Compatible
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 392 amino acids
TYPE: amino acid
 Query Match
Best Local Similarity 98.43
Matches 377; Conservative
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 TELEFAX: 206-442-6678
 MOLECULE TYPE: protein FRAGMENT TYPE: internal
 NAME: Parker, Gary E
REGISTRATION NUMBER:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
 single
 COMPUTER: IBM CON OPERATING SYSTEM:
 linear
 CLASSIFICATION:
 Seattle
 STRANDEDNESS:
 FILING DATE:
 COUNTRY: US
ZIP: 98102
 FILING DATE
 TELEPHONE:
 TOPOLOGY:
 RESULT 12
JS-09-072-384-2
 STATE:
 181
 TELEX:
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 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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 Gaps
 ö
 Length 392;
 Indels
 ; Score 2080; DB 3;
; Pred. No. 5.6e-220;
0; Mismatches 0;
 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
 ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 iTPLKYAQICYWIKGNYLDCREG 383
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PARKEY, GATY E
REGISTRATION NUMBER: 31,648
REFERENCE/DOCKET NUMBER: 97-1,
TELEPOMNUICATION INFORMATION:
TELEPHONE: 206-442-6673
TELEPHONE: 206-442-6673
 Query Match
Best Local Similarity 100.0%;
Matches 383; Conservative 0
 INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
 NAME/KEY: Signal Sequence
LOCATION: 1...19
OTHER INFORMATION:
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 MOLECULE TYPE: protein
FRAGMENT TYPE: internal
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
 TYPE: amino acid
STRANDEDNESS: single
 ORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
 TOPOLOGY: linear
 FILING DATE:
CLASSIFICATION:
 USA
 98102
 COUNTRY:
 US-09-072-384-15
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 Gaps
Sequence 2, Application US/09072384

Patent No. 6153420

GENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: SERINE PROTEASE POLYPEPTIDES

TITLE OF INVENTION: AND MATERIALS AND METHODS FOR MAKING THEM
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ANDRESS:

ADDRESSEE: ZymoGenetics, Inc.

STREET: 1201 Eastlake Avenue East
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 Length 392;
 Indels
 Score 2044; DB 3;
Pred. No. 5.1e-216;
1; Mismatches 5;
 OPERATING SYSTEM: DOS
CURFUARRE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,384
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TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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 59; Gaps
 APPLICANT: No. 6558939regaard-Madsen, Mads
APPLICANT: Octergaard, Peter Rahbek
APPLICANT: Christensen, Claus Bo Voge
APPLICANT: Lassen, Soren Flensted
TITLE OF INVENTION: No. 6558939el Proteases And Variants Thereof
FILE REFERENCE: 5665.200-US
CURRENT APPLICATION UNDHER: US/09/551,826D
CURRENT FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Version 3.2
SEQ ID NO 6
 GENERAL INFORMATION:
APPLICANT: No. 6558939regaard-Madsen, Mads
APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Christensen, Claus Bo Voge
APPLICANT: Assen, Soren Flensted
TITLE OF INVENTION: No. 6558939el Ptoteases And Variants Thereof
FILE REFERENCE: 5665.200-US
 Query Match
9.7%; Score 202.5; DB 4; Length 314;
Best Local Similarity 24.8%; Pred. No. 2e-13;
Matches 77; Conservative 37; Mismatches 137; Indels 59
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US-09-551-826D-6
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 Sequence 6, Application US/09551826D
Patent No. 6558939
 Sequence 2, Application US/09551826D Patent No. 6558939
 363 PLKYAQICYW 372
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 GENERAL INFORMATION
 US-09-551-826D-6
 US-09-551-826D-2
 LENGTH: 314
TYPE: PRT
 361
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 ADDRESSEE: No. 5523237o No. 5523237disk of No. 5523237th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
 290 LVYRFCD---VKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKII----GIFSGH 343
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Matches 79; Conservative 43; Mismatches 143; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/090,048
FILING DATE: 16-JUL-1993
CLASSIFICATION: 435
 344 QWVDMNGSPQDFNVAVRITPLKYAQICYW 372
 -----SSYNRGTRITKEVFDNLTNW 311
 GENERAL INFORMATION:
APPLICANT: Budtz, Peter
APPLICANT: Nielben, Per M.
ATITLE OF INVENTION: PROTEIN PREPARATIONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CURRENT APPLICATION NUMBER: US/09/551,826D CURRENT FILING DATE: 2000-04-17 NUMBER OF SEQ ID NOS: 14 SOSTWARE: Patentin version 3.2 SEQ ID NO 2
 STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00036
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
 Sequence 1, Application US/08090048
Patent No. 5523237
 LENGTH: 316
TYPE: PRT
ORGANISM: Bacillus licheniformis
 NAME: Agris, Cheryl H. REGISTRATION NUMBER: 3
 US-09-551-826D-2
 RESULT 15
US-08-090-048-1
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8.5%; Score 177; DB 1; Length 222;
Best Local Similarity 25.5%; Pred. No. 7.3e-11;
Matches 60; Conservative 27; Mismatches 104; Indels 44; Gaps
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REFERENCE/DOCKET NUMBER: 3396.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-090-048-1
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Search completed: July 1, 2005, 21:10:44 Job time : 26.9272 secs

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July 1, 2005, 21:08:25; Search time 88.2836 Seconds (without alignments) 1673.692 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1722976 seqs, 385795295 residues
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 OM protein - protein search, using sw model
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 US-09-658-677-18
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Perfect score:
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| 261,<br>261,<br>261,<br>261,<br>261,<br>261,<br>261,<br>261,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| esquence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>seq |
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## ALIGNMENTS

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 Gарв
 APPLICANT: Cao, Li
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458-0104/200130-449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
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0
 100.0%; Score 2080; DB 9; Length 383; 100.0%; Pred. No. 1.2e-194; ive 0; Mismatches 0; Indels 0
 ; Sequence 12, Application US/09765205; Patent No. US20020034800A1; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.
Matches 383; Conservative
 TYPE: PRT
ORGANISM: human
US-09-765-205-12
 US-09-765-205-12
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PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-11-30
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PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09909088B Patent No. US20020146709A1 GENERAL INFORMATION:
 Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Query Match 100.
Best Local Similarity 100.
Matches 383; Conservative
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; ORGANISM: Homo Sapien
US-09-909-320-261
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 APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart. Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION UNBER: US 60/143,048
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
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 APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
 APPLICATION NUMBER: PCT/US99/28214
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
 Godowski, Paul J.
Grimaldi, Christopher J.
 Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerber, Hanspeter
Gerritsen, Mary E
 Gurney, Austin L.
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
Gao, Wei-Qiang
 Goddard, A.
 121
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 181
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 APPLICANT:
APPLICANT:
APPLICANT:
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Goddard, A.
 Рап, Јашев
 JS-09-905-291A-261
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 APPLICANT:
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APPLICANT:
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 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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 Transmembrane Polypeptides and Nucleic
 Gaps
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 Length 383;
 Indels
 1.2e-194;
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 DB 9;
 Query Match
100.0%; Score 2080; 1
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 383; Conservative 0; Mismatches
 APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
 PRIOR FILING DATE: 2001-07-120
PRIOR FILING DATE: 2000-02-22
PRIOR PELLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USO(04414
PRIOR PLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PRIOR FILING DATE: 1999-09-08
PRIOR PELICATION NUMBER: PCT/US99/2054
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
 PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US09/00219
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 383
 APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
 APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
Grimaldi, Christopher J.
 Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Kenneth, J
 Kljavin, Ivar J.
Mather, Jennie P.
 Nicholas F.
 Pan, James
 TYPE: PRT

ORGANISM: Homo Sapien

US-09-909-088B-261
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KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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 241 IGMDYDYALLELKKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Stewart, Timethy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
 301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 CURRENT APPLICATION NUMBER: US/09/905,291A CURRENT FILING DATE: 2001-07-12 PRIOR PAPLICATION NUMBER: US/09/905,291A PRIOR PAPLICATION NUMBER: US/04/14 PRIOR FILING DATE: 2000-02-2 PRIOR PELING DATE: 1999-07-07 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR FILING DATE: 1999-07-26 PRIOR PILING DATE: 1999-09-08 PRIOR PILING DATE: 1999-09-08 PRIOR FILING DATE: 1999-09-13 PRIOR PILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: PCT/US99/21090 PRIOR PILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: PCT/US99/21647 PRIOR APPLICATION NUMBER: PCT/US99/21647 PRIOR APPLICATION NUMBER: PCT/US99/21647 PRIOR APPLICATION NUMBER: PCT/US99/21080 PRIOR PILING DATE: 1999-10-05 PRIOR PILING DATE: 1999-10-05 PRIOR PILING DATE: 1999-10-05 PRIOR PILING DATE: 1999-11-29
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09905291A Patent No. US20020160374A1 GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Gurney, Austin L.
Hillan, Kenneth, J.
 Gerber, Hanspeter
Gerritsen, Mary E
 Kljavin, Ivar J.
Mather, Jennie P.
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L
 Fong, Sherman
Gao, Wei-Qiang
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TITLE REPRENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902,853

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US/09/65,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-20

PRIOR FILING DATE: 1999-12-02

PRIOR PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-02

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PRIOR PRIOR FILING DATE: 1999-12-02

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Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Stewart, Timothy A. Tumas, Daniel
 Paoni, Nicholas F.
Roy, Margaret Ann
 Query Match 100.
Best Local Similarity 100.
Matches 383; Conservative
 Pan, James
 TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-261
 121
 121
 APPLICANT:
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 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
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 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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 Length 383;
 Indels
 Query Match 100.0%; Score 2080; DB 9; Best Local Similarity 100.0%; Pred. No. 1.2e-194; Matches 383; Conservative 0; Mismatches 0;
 FRIOR FILING DATE: 1999-12-30

PRIOR FILING DATE: 1999-12-02

PRIOR PELLOATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR PELLOR DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-20

PRIOR PELLOR DATE: 1999-12-20

PRIOR PELLOR DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/3099

PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 1999-12-30

PRIOR FILING DATE: 1999-12-30

PRIOR FILING DATE: 1999-12-30

PRIOR PILING DATE: 1999-12-30

PRIOR PILING DATE: 1999-12-30

PRIOR PILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

LENGTH: 383
APPLICATION NUMBER: PCT/US99/28313
 Sequence 261, Application US/09902853
GRUBLAGATION US2020192659A1
GRUBLAGATION
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Persno, David
APPLICANT: Fernara, Napoleone
APPLICANT: Fernara, Napoleone
APPLICANT: Fernara, Napoleone
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferraza, Napoleone
Filvaroff, Ellen
Fong, Sherman
 Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 LING DATE: 1999-11-30
 ; ORGANISM: Homo Sapien
US-09-905-291A-261
 Goddard, A.
 US-09-902-853-261
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 APPLICANT:
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 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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 1 MAGIPGLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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0
 Length 383;
 0; Indels
 100.0%; Score 2080; DB 9;
100.0%; Pred. No. 1.2e-194;
ative 0; Mismatches 0;
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 Length 383;
 Indels
 Query Match
100.0%; Score 2080; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 383
 Sequence 261, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Destsein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
 , ORGANISM: Homo Sapien
US-09-907-824-261
 RESULT 7
US-09-907-841-261
 APPLICANT:
APPLICANT:
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 301
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 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
 CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR APLICATION NUMBER: 09/665,350
PRIOR APLICATION NUMBER: PCT/USO0/04414
PRIOR PILING DATE: 2000-02-22
PRIOR PILING DATE: 1990-07-07
PRIOR PLLING DATE: 1990-07-07
PRIOR PLILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
 PPLICATION NUMBER: PCT/US99/23089
LING DATE: 1999-10-05
 APPLICATION NUMBER: PCT/US99/28214
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Application US/09907824
5. US20020197671A1
 Godowski, Paul J.
Grimaldi, Christopher J.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Gurney, Austin L.
Hillan, Kenneth, J
 Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 Kljavin, Ivar J.
Mather, Jennie P.
 Goddard, A.
 Pan, James
 Sequence 261, Applic
Publication No. US2(
GENERAL INFORMATION
 Pong,
 181
 241
 301
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APPLICANT:
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 301 TYDLLYQQCDAQPGASGSGVYVRWWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
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 FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,841

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 2001-02-2

PRIOR PILING DATE: 2001-02-2

PRIOR PLING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PLING DATE: 1999-09-09

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

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PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-29
 APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 1 MAGIPGLLFLLFFLLCAVGOVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGABAKLB
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 0; Gaps
 Length 383;
 0; Indels
 Query Match 100.0%; Score 2080; DB 9; Best Local Similarity 100.0%; Pred. No. 1.2e-194; Matches 383; Conservative 0; Mismatches 0;
Grimaldi, Christopher J
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
Roy, Margaret Ann
 ORGANISM: Homo Sapien
 US-09-907-841-261
 181
 APPLICANT:
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APPLICANT:

APPLICANT:

Wood, William, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/04.011

CURRENT APPLICATION NUMBER: US/09/05.130

PRIOR PLING DATE: 2000-09-18

PRIOR PLING DATE: 1999-00-06

PRIOR PLING DATE: 1999-00-26

PRIOR PLING DATE: 1999-00-26

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PRIOR PLING DATE: 1999-00-36

PRIOR PLING DATE: 1999-09-09

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PRIOR PLING DATE: 1999-10-15

PRIOR PLING DATE: 1999-10-16

61 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Williams, P. Mickey Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Gurney, Austin L.
Hillan, Kenneth, J
 Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 Paoni, Nicholas F
 Kljavin, Ivar J.
Mather, Jennie P.
 Ashkenazi, Avi
Botstein, David
 Desnoyers, Luc
Eaton, Dan L.
 APPLICANT: Genentech, Inc
 Pan, James
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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FITLE OF INVENTION: Acids Encoding the Same FILLE PERERNCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,640
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
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LENGTH: 383
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 Length 383;
 Indele
 100.0%; Score 2080; DB 10;
100.0%; Pred. No. 1.2e-194;
ative 0; Mismatches 0;
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAOICYWIKGNYLDCREG 383
 Sequence 261, Application US/09908093
Publication No. US20030017498A1
GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 Gurney, Austin L.
Hillan, Kenneth, J
 Paoni, Nicholas F
Roy, Margaret Ann
 Kljavin, Ivar J.
Mather, Jennie P.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Matches 383; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 Рап, Јашев
 Query Match
Best Local Similarity
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 US-09-908-093-261
 APPLICANT:
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 121
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 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG 180
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 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQMIRVKRTHVPKGWIKGNAND
 Gaps
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 vuery match 100.0%; Score 2080; DB 10; Length 383; Best Local Similarity 100.0%; Pred. No. 1.2e-194; Matches 383; Conservative 0; Mismatches Λ. τ-2-1
 PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
LENGTH: 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09903640 Publication No. US20030017463A1 GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A.
 Gerritsen, Mary E
 Tong, Sherman
Sao, Wei-Qiang
 APPLICANT: Genentech, Inc.
 Stewart, Timot
Tumas, Daniel
 Goddard, A.
 TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-261
 Рап, Јашев
 US-09-903-640-261
 APPLICANT:
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APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: 10466-14

FILE REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,742

CURRENT FILING DATE: 2001-07-16

PRIOR PLILING DATE: 2000-09-18

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PRIOR PLILING DATE: 2000-09-18

PRIOR PLILING DATE: 1999-07-07

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PRIOR PLILING DATE: 1999-11-30

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 361 ITPLKYAQICYWIKGNYLDCREG 383
 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09906742
Publication No. US20030023054A1
 Godowski, Paul J.
Grimaldi, Christopher J.
 Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 Gurney, Austin L.
Hillan, Kenneth, J.
 Paoni, Nicholas F.
Roy, Margaret Ann
 Kljavin, Ivar J.
Mather, Jennie P.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Goddard, A.
 Pan, James
 GENERAL INFORMATION
 US-09-906-742-261
 301
 361
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/908,093
CURRENT FILING DATE: 2001-07-17
PRIOR PAPLICATION NUMBER: PCT/USO0/0414
PRIOR PLING DATE: 2000-09-18
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 Score 2080; DB 10; Length 383;
Pred. No. 1.2e-194;
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100.0%; Score 2080; I
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 383; Conservative 0; Mismatches
 PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-20
PRIOR APLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGHH: 383
 R FILING DATE: 1999-09-13
R APPLICATION NUMBER: PCT/US99/21090
R FILING DATE: 1999-09-15
R FILING DATE: 1999-09-15
R FILING DATE: 1999-09-15
R APPLICATION NUMBER: PCT/US99/21049
R FILING DATE: 1999-10-05
R APPLICATION NUMBER: PCT/US99/28214
R FILING DATE: 1999-11-29
R FILING DATE: 1999-11-29
R FILING DATE: 1999-11-29
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-908-093-261
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PAPLICANTE WOOD, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FITLE OF INVENTION: Acids Encoding the Same CURRENT FILMS OF 1266-136
FILMS APPLICATION NUMBER: US/09/906,838
CURRENT FILMS DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR PELICATION NUMBER: PCT/US00/0414
FRIOR PELICATION NUMBER: PCT/US09/0414
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-26
FRIOR FILING DATE: 1999-07-28
FRIOR FILING DATE: 1999-01-38
FRIOR FILING DATE: 1999-11-30
FRIOR FILING DATE: 1999-11-20
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FRIOR FILING DATE: 1999-11-20
FRIOR APPLICATION NUMBER: PCT/US99/2091
FRIOR FILING DATE: 1999-11-20
FRIOR FRIOR FRIOR DATE: 1999-11-20
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 100.0%; Score 2080; DB 10; Length 383; 100.0%; Pred. No. 1.2e-194; ive 0; Mismatches 0; Indels 0;
 Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A
 aoni, Nicholas F.
 Query Match
Best Local Similarity 100.
Matches 383; Conservative
 Tumas, Daniel
 , ORGANISM: Homo Sapien
US-09-906-838-261
 121
 181
 APPLICANT:
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 240
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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 Query Match
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Best Local Similarity 100.0%; Pred. No. 1.2e-194;
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Sequence 261, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Kenneth, J
 Gerber, Hanspeter
Gerritsen, Mary E
 Gurney, Austin L.
Hillan, Kenneth,
 APPLICANT: Genentech, Inc.
APPLICANT: Abhkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L.
APPLICANT: Eaton, Dan L.
 Kljavin, Ivar J
 Mather, Jennie
 Wei-Qiang
 Sherman
 Goddard, A.
 ; ORGANISM: Homo Sapien
US-09-906-742-261
 Fong,
 US-09-906-838-261
 121
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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 APPLICANT
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241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
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 1 MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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 Length 383;
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100.0%; Score 2080; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PRILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 261
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
 Sequence 261, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
 Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-907-613-261
 US-09-907-942-261
 APPLICANT:
APPLICANT:
APPLICANT:
 181
 APPLICANT:
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 APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,613

CURRENT PILING DATE: 2001-07-17

PRIOR PILING DATE: 2000-02-22

RIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

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PRIOR PILING DATE: 1999-11-30

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 Sequence 261, Application US/09907613
PUblication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Besteein, David
APPLICANT: Desnoyers, Luc
 361 ITPLKYAQICYWIKGNYLDCREG 383
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
 Gerber, Hanspeter
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 Kljavin, Ivar J.
Mather, Jennie P.
 Wei-Qiang
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 US-09-907-613-261
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 IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
 TILE CF. LING DATE: ACIDE ELCCAING THE SAME CURRENT APPLICATION NUMBER: US/09/904,859 CURRENT APPLICATION NUMBER: US/09/904,859 CURRENT FILING DATE: 2001-07-12 PRIOR FILING DATE: 2000-09-16 PRIOR FILING DATE: 2000-09-16 PRIOR PELICATION NUMBER: US 60/143,048 PRIOR FILING DATE: 1999-07-26 PRIOR APPLICATION NUMBER: US 60/146,222 PRIOR APPLICATION NUMBER: US 60/146,222 PRIOR PELING DATE: 1999-07-26 PRIOR PELING DATE: 1999-07-26 PRIOR PELING DATE: 1999-07-26 PRIOR FILING DATE: 1999-07-28 PRIOR FILING DATE: 1999-07-28 PRIOR FILING DATE: 1999-09-13 PRIOR FILING DATE: 1999-09-15 PRIOR FILING DATE: 1999-09-15 PRIOR FILING DATE: 1999-09-15 PRIOR FILING DATE: 1999-10-05 PRIOR FILING DATE: 1999-10-05 PRIOR FILING DATE: 1999-10-05 PRIOR FILING DATE: 1999-11-29 PRIOR FILING DATE: 1999-11-29 PRIOR FILING DATE: 1999-11-30 PRIOR FILING DATE: 1999-11-30 PRIOR FILING DATE: 1999-11-30
 361 ITPLKYAQICYWIKGNYLDCREG 383
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 Sequence 261, Application US/09904859
Publication No. US20030036060A1
GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Williams, P. Mickey Wood, William, I.
 Kenneth, J
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerber, Hanspeter
Gerritsen, Mary E
 Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Iuc
 Gurney, Austin L.
 Kljavin, Ivar J.
Mather, Jennie P.
 Fong, Sherman
Gao, Wei-Qiang
 Eaton, Dan L.
 Goddard, A.
 Рап, Јашев
 RESULT 15
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 APPLICANT:
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 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
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 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND 240
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 IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
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 Gaps
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 Query Match 100.0%; Score 2080; DB 10; Length 383; Best Local Similarity 100.0%; Pred. No. 1.2e-194; Matches 383; Conservative 0; Mismatches 0; Indels 0;
 CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT APPLICATION NUMBER: US/09/907,942
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PRIOR FILING DATE: 1999-12-16
PRIOR PPLICATION NUMBER: PCT/US99/30911
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PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 383
 PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PELICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
 APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15 APPLICATION NUMBER: PCT/US99/21547
 Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
 FILING DATE: 1999-09-15
Mather, Jennie P.
 TYPE: PRT
ORGANISM: Homo Sapien
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 KTYVKGTOKLRVGPLKPKFKDGGRGANDSTSAMPEQMKFOWIRVKRTHVPKGWIKGNAND 240
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIXILSSSGDGAQHRDSGS 120
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100.0%; Score 2080; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.2e-194;
Matches 383; Conservative 0; Mismatches 0; Indels 0;
| PRIOR APPLICATION NUMBER: PCT/US99/28564 |
| PRIOR FILING DATE: 1999-12-02 |
| PRIOR PLING DATE: 1999-12-02 |
| PRIOR PLING DATE: 1999-12-02 |
| PRIOR PLING DATE: 1999-12-16 |
| PRIOR PLING DATE: 1999-12-16 |
| PRIOR PLILOR DATE: 1999-12-16 |
| PRIOR PLILOR DATE: 1999-12-20 |
| PRIOR PLILOR DATE: 1999-12-30 |
| PRIOR PLILOR DATE: 1999-12-30 |
| PRIOR PLILOR DATE: 2000-01-05 |
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OM protein - protein search, using sw model

July 1, 2005, 20:54:23 ; Search time 20.3479 Seconds (without alignments) 1811.048 Million cell updates/sec Run on:

US-09-658-677-18 2080 1 MAGIPGLLFPLLCAVGQ......LKYAQICYWIKGNYLDCREG 383

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | endopeptidase (EC | metalloproteinase | choline binding pr | fact  | pancreatic elastas | hypothetical prote | pancreatic elastas |        | pancreatic elastas | probable pancreati | trypsin-like prote | choline binding pr | complement factor | pancreatic elastas | pancreatic elastas | trypsin (EC 3.4.21 | hypothetical prote | Putative protease | coagulation factor | brain-specific ser | pancreatic elastas | coagulation factor | hypothetical prote | probable secreted | probable pepetidas | complement factor | serine proteinease | masquerade precurs | T-cell suppressor |
|-----------|----------------|-------------------|-------------------|--------------------|-------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|-------------------|
| SUMMARIES | ΩI             | A45134            | A35122            | E97915             | EXRT  | A26823             | T29767             | B26823             | A25528 | S70439             | A56615             | TRWVSY             | C95045             | DBHU              | ELPG               | ELRT1              | TRSMG              | E85765             | H64915            | EXHU               | JC5759             | C26823             | EXBO               | T15308             | T35117            | AH0282             | A29154            | A47547             | A55617             | A28566            |
|           | DB             |                   | ~                 | ~                  | Н     | ~                  | ~                  | ~                  | N      | 4                  | 4                  | Н                  | N                  | Н                 | Н                  | н                  | н                  | ~                  | ~                 | Н                  | ~                  | ~                  | -                  | ~                  | N                 | ~                  | 7                 | -                  | ~                  | ~                 |
|           | Length         | 316               | 313               | 218                | 482   | 269                | 522                | 269                | 271    | 258                | 267                | 238                | 285                | 246               | 266                | 266                | 259                | 273                | 273               | 488                | 761                | 269                | 492                | 1582               | 405               | 278                | 583               | 786                | 1047               | 236               |
| dip       | Query<br>Match | 9.3               | 6.5               | 6.3                | 8     | 5.7                | 5.6                | 5.6                | 9.9    | S                  | •                  | 5.5                | 5.5                | 5.5               | 5.4                | 5.4                | 5.4                | 5.4                | 5.4               | 5.4                | 5.3                | 5.3                | 5.3                | 5.3                | 5.3               | 5.2                | 5.2               | 5.2                | 5.5                | 5.2               |
|           | Score          | 194               | 135.5             | 131                | 120.5 | 119                | 117                | 115.5              | 115.5  | 115                | 115                | 114.5              | 114.5              | 114               | 113                | 113                | 112.5              | 112.5              | 112.5             | 111.5              | 111                | 110                | 110                | 110                | 109.5             | 109                | 108               | 108                | 108                | 107.5             |
|           | Result<br>No.  | 1                 | 7                 | e                  | 4     | w                  | 9                  | 7                  | ω      | O                  | 10                 | 11                 | 12                 | 13                | 14                 | 15                 | 16                 | 17                 | 18                | 19                 | 20                 | 21                 | 22                 | 23                 | 24                | 25                 | 56                | 27                 | 28                 | 29                |

| Ra-reactive factor | trypsin-related pr | pancreatic elastas | coagulation factor | hypothetical prote | trypsin-like prote | trypein (EC 3.4.21 | probable trypsin V | probable polygalac | membrane-bound arg | probable secreted | coagulation factor | complement factor | coagulation factor | allergen Der f III | factor IX - rabbit |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| A59271             | 840004             | ELRT2              | KFBO               | T34929             | JC4170             | S40006             | D82175             | T02289             | JC7731             | T35118            | A30351             | 151579            | A38738             | 568424             | 146712             |
| н (                | N                  | -                  | н                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                  | ~                 | -                  | 7                 | ~                  | ~                  | 7                  |
| 686                | 274                | 271                | 416                | 1238               | 272                | 267                | 548                | 624                | 855                | 409               | 452                | 747               | 1019               | 259                | 275                |
| 2.5                | 5.0                | 5.0                | 5.0                | 4.9                | 4.8                | 4.7                | 4.7                | 4.7                | 4.7                | 4.7               | 4.7                | 4.7               | 4.7                | 4.6                | 4.6                |
|                    |                    |                    |                    |                    | 0                  | D.                 | œ                  | 98                 | 8                  | 'n                | S                  | S                 | _                  | S                  |                    |
| 107.5              | 105                | 103.5              | 103.5              | 102.5              | 100                | 98.5               | o                  | •                  | o                  | 97.               | 97.                | 97.5              | 0,                 | 96                 | 96.5               |

## ALIGNMENTS

| <br>RESULT 1 A45134 endopeptidase (EC 3.4), glutamate-specific - Bacillus licheniformis                                                                    | . licheniformis                     |
|------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------|
| C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004 C;Accession: A45134; S23078                                                    |                                     |
| <br>R;Kakudo, S.; Kikuchi, N.; Kitadokoro, K.; Fujiwara, T.; Nakamura, E.; Okamoto, H.;<br>J. Biol. Chem. 267, 23782-23788, 1992                           | Nakamura, E.; Okamoto, H.; Shin,    |
| <br>A; Title: Purification, characterization, cloning, and expression of a glutamic acid-speci<br>A; Reference number: A45134; MUID:93054737; PMID:1429718 | vression of a glutamic acid-speci   |
| A; Accession: A43.13.4 A; Status: preliminary A; Molecule type: DNA                                                                                        |                                     |
| A;ReBiddes: 1-316 cAAA.><br>A;Cross-references: UNIPROT:P80057; GB:D10060; NID:g216263; PIDN:BAA00949.1; PID:d100141E                                      | 3; PIDN:BAA00949.1; PID:d100141E    |
| A; Note: gequence extracted from NCBI backbone (NCBIN:118784, NCBIP:118785)                                                                                | 784, NCBIP:118785)                  |
| <br>K;SVendsen, 1.; Breddam, K.<br>Eur. J. Biochem. 204, 165-171, 1992                                                                                     |                                     |
| <br>A; Title: Isolation and amino acid sequence of a glutamic acid specific endopeptidase from A; Reference number: S23078; MUID:92155199; PMID:1346764    | acid specific endopeptidase from    |
| A;Accession: S23078 A:Status: preliminary                                                                                                                  |                                     |
| A, Molecule type: protein A, Residues: 95-316 < SVE>                                                                                                       |                                     |
| <br>C;Superfamily: Glutamyl endopeptidase, V8 type<br>C;Keywords: hydrolase                                                                                |                                     |
| <br>Query Match 9.3%; Score 194; DB 2; Leng<br>Best Local Similarity 24.0%; Pred. No. 1.7e-08;<br>Matches 79; Conservative 43; Mismatches 143; Ir          | Length 316;<br>Indele 64; Gape 15;  |
| <br>Qy 63 SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSG                                                                                        | JIXILSSSGDGAQHRDSG 119              |
| Db 28 AQAAPSPHTPVSSDPSY-KAETSVTYDPNIKSDQYGLYSKAFTGTGKVNETKE                                                                                                | :  : :    :<br>LYSKAFIGIGKVNETKE 79 |
| Qy 120 SSGKSRRKRQIYGYDSRPSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHV                                                                                                 | STGCTGTLVAEKHV 170                  |
| Db 80 KAEKKSPAKAPYSIKSVIGSDDRTRVTNTTAYPYRAIVHISSSIGSCTGWMIGPKTV                                                                                            | SSSIGSCTGWMIGPKTV 136               |
| Qy 171 LTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHV                                                                                        | MPEQMKFQWIRVKRTHV 229               |
| Db 137 ATAGHCIYDISSGSFAGTATVSPGRNGTSYPYGSVKSTRYFI                                                                                                          | YPYGSVKSTRYFI 178                   |
| Qy 230 PKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGN                                                                                        | PGGRIHFSGYDNDRPGN 289               |
| Db 179 PSGWRSGNTNYDYGAIELSEPIGNTVGYFGYSYTTSSLVGTTVTISGYFGDKTAG                                                                                             | VGTTVTIŠGYPGDKTAG 233               |
| Qy 290 LVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGH                                                                                              | KWERKIIGIFSGH 343                   |
| Db 234 TQWQHSGPIAISETYKLQYAM-DTYGGQSGSPVFEQSSSRTNCSGPCSLAVHTNGGYGG-                                                                                        | SGPCSLAVHŢNGVYGG- 291               |

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| Qy 344 QWVDMNGSPQDFNVAVRITPLKYAQICYW 372<br>:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Db 176 -SGTMFYSVK-GWTESKDTNYDYGAIKLNGSPGNTVGW-YGYRTTNSSSPVGL 225                                                                                                                                                                    |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Db 226 SSSVTGFPCDKIFGTMWSDTKPIRSAETYKLTY-TTDTYGCQSGSPVY 27                                                                                                                                                                          |
| A35127<br>Catalloproteinase (EC 3.4) mpr precursor, extracellular - Bacillus subtilis<br>C;Species: Bacillus subtilis<br>C;Date: 27-Jul-1990 #sequence revision 27-Jul-1990 #text change 16-Aug-2004                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Qy 326 KRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW 372<br>                                                                                                                                                                      |
| C;Accession: A35122; I40010; Ā69660<br>R;Sloma, A.; Rudolph, C.F.; Rufo Jr., G.A.; Sullivan, B.J.; Theriault, K.A.; Ally, D.; F<br>J. Bacteriol. 172. 1024-1029. 1990                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RESULT 3                                                                                                                                                                                                                            |
| A;Title: Gene encoding a novel extracellular metalloprotease in Bacillus subtilis. A;Reference number: A35122; MUID:90130256; PMID:2105291 A;Accession: A35122                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | E97915<br>choline binding protein G, truncation [imported] - Streptococcue<br>C;Species: Streptococcus pneumoniae                                                                                                                   |
| A;Status: preliminary<br>A;Molecule type: DNA<br>A;Residues: 1-313 <5LO><br>A;Cross-references: INIDROM: D39790. GB:110505. NID: <1412009. DIDN: Aba225604 1. DTD:3143210                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                     |
| R;Smith, H.; de Jong, A.; Bron, S.; Venema, G. Gene 70, 351-361, 1988 A;Title: Characterization of signal-sequence-coding regions selected from the Bacillus statements number. 134904. MITD. 491,0019. DATE. 214506.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | y, P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001 A; Abtubors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, a.m.t.le. Ganome of the Bacterium Streathonorums naminale Strain R6         |
| A; Accession: I40010 A; Status; preliminary; translated from GB/EMBL/DDBJ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | A; Reference number: A97872; MUID:21429245; PMID:11544234<br>A; AAccession: B97915                                                                                                                                                  |
| A; Residues: 1-60,65,'L',67,'S',69,'AQA' <res> A; Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702 A; Cross-references: GB:M22916; NID:g143701; PIDN:AAA22832.1; PID:g143702 C: Browistan, N:, Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C: Browislan, C: Browner, C: Bro</res> | A;Molecule type: DNA<br>A;Molecule type: DNA<br>A;Residues: 1-218 <kur><br/>A;Cross-references: UNIPROT:Q8DR41; GB:AE007317; PIDN:AAK99153.1; PID:g15457907; GSPDB:GA</kur>                                                         |
| A.; Bhlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | À                                                                                                                                                                                                                                   |
| A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Query Match 6.3%; Score 131; DB 2; Length 218;<br>Best Local Similarity 24.2%; Pred. No. 0.0019;<br>Matches 59; Conservative 30; Mismatches 87; Indels 68; Gaps 10;                                                                 |
| A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Oy 14                                                                                                                                                                                                                               |
| Ajaucnois: Schletch, S.; Schroeter, K.; Scotione, F.; Sekigichi, J.; Sekowska, A.; Seron<br>akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,<br>T. Winters D. Winst B. Vamanoto H. Vamanot K. Vasumoto K. Varia K. Varia K. Vochida M                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | DD 5 DNILQIFYSISAMVLSNXIGVALGGGNVBGRGSANFILANNILIAANNITR                                                                                                                                                                            |
| A. Authors: Yoshikawa, H.F.; Zumatein, B.; Yoshikawa, H.; Danchin, A. A.File: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | DD 55HDYGKBADDIYULPAVSPSQELFGKIKVKEVRYLKEFRNINSKD-AREYD                                                                                                                                                                             |
| A; Reletence number: A09500; MULD: 980444033; FMLD: 9384377<br>A; Accession: A69660 nucleic acid sequence not shown; translation not shown<br>A; Status: preliminary; nucleic acid sequence not shown<br>A; Molecule type: DNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Qy 247 YALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300                                                                                                                                                                   |
| A;Residues: 1-313 <kun> A;Residues: 1-313 <kun> A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12018.1; PID:e1182176; A;Experimental source: strain 168 C;Genetics:</kun></kun>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Qy 301 TYDLLYQQCDAQPQASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNV 357  Db 157 LSDGWFLDYGVDTLESSGSTYYDASHRVVGYTLGDGANOINS 201                                                                                                         |
| A;Gene: mpr<br>C;Superfamily: Glutamyl endopeptidase, V8 type                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | AVRI 361                                                                                                                                                                                                                            |
| Query Match 6.5%; Score 135.5; DB 2; Length 313;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Db 202 AVKL 205                                                                                                                                                                                                                     |
| best bocal Similarity 42.2%; Fred. NO. 0.0013; Matches 77; Conservative 38; Mismatches 121; Indels 111; Gaps 17;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | RESULT 4                                                                                                                                                                                                                            |
| Qy 72 GFPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRRKQ 129                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Coagulation factor Xa (EC 3.4.21.6) precursor - rat<br>C;Species: Rattus norvegicus (Norway rat)<br>C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004                                                     |
| Qy 130 IYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTL 164                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | C,Accession: 3490/3; 0446/0/; FS0131; FS0130; 102/43<br>F)Stanton, C. Ross, P.; Hutson, S.; Wallin, R.<br>Thromb. Res. 80, 63-73, 1995<br>A;Title: Evidence for competition between vitamin K-dependent clotting factors for intrac |
| 165 VAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGAND :   :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | m                                                                                                                                                                                                                                   |
| DD 136 VNPNTVVTAGHCVYSQDHGWASTITAAFGKNGSSYFYGIY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | A;Kossiques: 1-482 CSTAL><br>A;Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g5066(<br>A;Note: submitted to the EMBL Data Library, June 1994                                                     |

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A;Realdues: 1-522 <WAT>
A;Cross-references: UNIPROT:001771; EMBL:AF003134; PIDN:AABS4144.1; GSPDB:GN00019; CESP:?
A;Experimental source: strain Bristol N2; clone 2C581
 A,Accession: A26823
A,Molecule type: mRNA
A,Residues: 1-269 <KRAW>
A,Cross-references: UNIPROT:P08419; GB:M16651; NID:g164441; PIDN:AAA31027.1; PID:g164442
A,Cross-references: UNIPROT:P08410; CB:M16651; NID:g164441; PIDN:AAA31027.1; PID:g164442
C,Superfamily: trypsin; trypsin homology
C,Reywords: hydrolase; serine proteinase
F;1-16/Domain: signal sequence #status predicted <SIG>
F;77-28/Domain: propeptide #status predicted <PRO>
F;77-28/Product: elastase II #status predicted <MAT>
F;29-262/Domain: trypsin homology <TRY>
F;39-262/Domain: trypsin homology <TRY>
F;73,121,216/Active site: His, Asp, Ser #status predicted
 two elastase II mRNAs are
 182 TY--VKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAN 239
 80 TYRVVLGRHSL------STNEPGSLA-----VKVSKLVVHQDW---NSN 114
 240 DIGMDYDYALLELKKP-HKRKFMKIGVSPPAKQ-LPG------GRIHFSGYDND--R 286
 115 QLSNGNDIALLKLASPVSLTDKIQLGCLPAAGTILPNNYVCYVTGWGRLQTNGASPDILQ 174
 -----KLSTGCTGTLVAEK 168
 142 PFFLKILEMILYWLRIPFSAKVYNGRDASQSEAPWSVFTYLYSKDEQSATTCTGTIVSPR 201
 28 RVVGGEDARPN-----SWPWQVSLQYDSSGQWRHTCGGTLVDQSWVLTAAHCISSSR 79
 Cispecies: Caenorhabditis elegans
Cibate: 15-0ct-1999 #text_change 09-Jul-2004
Cibate: 15-0ct-1999 #tequence_revision 15-0ct-1999 #text_change 09-Jul-2004
Cibacession: T29767
R;Waterston, B.; Gattung, S.; Le, T.T.
R;Waterston, B.; Gattung, S.; Le, T.T.
R;Waterston, B.; Gattung, S.; Le, T.T.
A;Description: The sequence of C. elegans cosmid 2C581.
A;Description: The sequence of C. elegans cosmid 2C581.
 128 RQIYGYDSRFSIFGKDFLLNYPFSTSVKL-STG-----CTGTLVAEKHVLTAAHCIHDGK
 26 KPSNKASSAPSLRKKSSSNPNKGTARSVSKSVPKSSAIPASPTVQKEVPPVEIEKKKEEK
 84 -----YLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRRKRQIYGYDSRF
 86 PENOKKELAEKKL----DRTQDDGKEYKEAESALGVVIKEDKAPAKMDDGYEDFGPGCEF
 29 KPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSS---CGPQCHKGTPLPTYEEAKQ--
 . 99
 Query Match 5.6%; Score 117; DB 2; Length 522; Best Local Similarity 20.4%; Pred. No. 0.082; Matches 95; Conservative 56; Mismatches 153; Indels 162;
 Query Match 5.7%; Score 119; DB 2; Length 269; Best Local Similarity 27.5%; Pred. No. 0.024; Matches 60; Conservative 28; Mismatches 64; Indels 6
 A;Introns: 36/2; 138/3; 234/2; 311/1; 331/1; 421/1; 470/2
 287 PGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRM 324
 175 QGQLL-----VVD-----YATC-SKPGWWGSTVKTNM 200
 R;Kawashima, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
DNA 6, 163-172, 1987
A;Title: Characterization of pancreatic elastase II CDN/
A;Reference number: A90958; MUID:87217962; PMID:3646943
 hypothetical protein ZC581.6 - Caenorhabditis elegans
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 SIFGKD----FLLNYPFSTSV-----
 Gene: CESP: ZC581.6
 A, Molecule type: DNA
 A; Accession: T29767
 RESULT 6
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Note: neither the complete nucleic acid sequence nor the complete translation are show Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601; Experimental source: Cos-1 cell; Enjyoji, K.; Miyazaki, K.; Kato, H.; Enjyoji, K.; Miyazaki, K.; Kato, H.; Enjyoji, K.; Miyazaki, K.; Miyazaki, M.; Kato, H.; Etichem. 109, 890-898, 1991; Fat factors X and Xa: demonstration of factor Xa in rat pla; PMID:1718949
 Function: catalyzes the proteolytic activation of prothrombin to thrombin in the propertipition: catalyzes the proteolytic activation of prothrombin to thrombin in the probathway: blood coagulation factor X; Edf homology, Gla domain homology; trypsin homology; Superfamily: coagulation factor X; Edf homology; Gla domain homology; trypsin homology; 1-23/Domain: signal sequence #status predicted <81G>.
24-40/Domain: gla domain homology <GLA>.
25-440/Domain: Gla domain homology <GLA>.
31-179/Promain: Edf homology <EGL>.
30-121/Domain: Edf homology <EGS>.
313-484/Pomain: Edf homology <EGS>.
313-484/Pomain: activation factor X heavy chain #status predicted <HCH>.
313-484/Pomain: activation peptide #status predicted <AFT>.
322-487/Product: coagulation factor Xa heavy chain #status predicted <ACT>.
 A; Molecule type: protein A; Residues: 183-186, X, 188-207 <ENJ2>
R; Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Bur. J. Haematol. 52, 162-168, 1994
A; Title: Analysis of the partial nucleotide sequences and deduced primary structures of A; Reference number: 146196; MUID:94222160; PMID:8168596
 A,Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs A,Reference number: JC4670; MUID:96194815; PMID:8647460
 160 CTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKF 219
 259 CGGTILNEFYILTAAHCLHQAKRF----KVRVGDLNTEQEDGGEMVHE-VDMIIKHNKF 312
 A26823

pancreatic elastase II (EC 3.4.21.71) precursor - pig
NiAlternate names: pancreatopeptidase B
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: A26823
 Gaps
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 295-383,'G',385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
 Length 482;
 Indels
 Query Match 5.8%; Score 120.5; DB 1; Best Local Similarity 32.3%; Pred. No. 0.038; Matches 31; Conservative 17; Mismatches 23;
 220 QWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP 255
 313 Q----RDTY-----329
 ,Accession: PS0191
;Wolecule type: protein
Residues: 41-58, X', 60-65 <ENJ1>
;Accession: PS0190
 Molecule type: mRNA;Residues: 1-482 <STA2>
 RESULT 5
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pancreatic elastase I (allele HEL1-16) probable splice form I - human C;Species: Homo sapiens (man)
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 28-Apr-2003
C;Accessinn: $70439
R;Kawashima, I.; Tani, T.; Mita-Honjo, K.; Shimoda-Takano, K.; Ohmine, T.; Furukawa, H.;
DNA, Seq. 2, 303-312, 1992
A;Title: Genomic organization of the human homologue of the rat pancreatic elastase I ger A;Reference number: A56615; MUID:92338395; PMID:1633328
 C;Accession: A25528
R;Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II
A;Reference number: A93646; MUID:87066713; PMID:3641189
 A;Cross-references: UNIPROT:P05208; GB:X04573; NID:950825; PIDN:CAA28242.1; PID:950826
C;Superfamily: trypsin homology
C;Superfamily: trypsin: proteinase
C;Superfamily: proteinase
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-27/Product: pancraatic elastase II #status predicted <MAT>
F;31-264/Domain: trypsin homology <TRY>
F;31-264/Domain: trypsin homology <TRY>
F;31-264/Domain: trypsin homology <TRY>
 147 NYPFSTSVKLSTG-----CTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFK 200
 201 DGGRG----ANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP- 255
 --GRHNLYVAESGSLA-----VSVSKIVVHKDW---NSNQISKGNDIALLKLANPV 131
 148 YPFSTSVK-LSTG-----CTGTLVAEKHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPKF 199
 200 KDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKP-HKR 258
 DVKDETY----DLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGS 351
 pancreatic elastase II (EC 3.4.21.71) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 SWPWQVSLQYSSNGKWYHTGGGSLIANSWVLTAAHCISSSRTY-----RVGL-----
 259 KFMKIGVSPPAKQ-LPGGRI-HFSGY-----DNDRPGNLV---YRFC----
 Gaps
 256 HKRKFMKIGVSPPAKQ-LPG-----GRIHFSGYDND--RPGNLV---YRFC 295
 83;
 DB 2; Length 271;
 Indels
 51;
 / Match 5.6%; Score 115.5; DB 2; Local Similarity 25.0%; Pred. No. 0.048; nes 67; Conservative 38; Mismatches 80;
 0.048;
28.6%; Preu.
 PODFNVAVRITPLKYAQICYWIKGNYLD 379
 -----NYID 262
 Conservative
 |: :| |::
PRKPSVFTRVS---
 Best Local Similarity
Matches 50; Conserv
 A; Molecule type: mRNA
A; Residues: 1-271 <STE>
 98
 352
 248
 93
 Query Match
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 Title: Primary structure of human pancreatic elastase 2 determined by sequence analysi
Reference number: A27432; MUID:88107669; PMID:3427074
 A;Molecule type: mRNA
A;Residues: 1-269 «KAW»
A;Cross-references: UNIPROT:P08217; GB:M16652; NID:g182057; PIDN:AAA52380.1; PID:g182058
R;Fletcher, T.S.; Shen, W.F.; Largman, C.
Biochemistry 26, 7256-7251, 1987
A;Title: Primary structure of human pancreatic elastase 2 determined by sequence analysi
 complexes involving procarboxype
 Cross-references: GB:M16631; NID:g182022; PIDN:AAAS2374.1; PID:g182023
Shirsau, Y.; Yoshida, H.; Matsuki, S.; Takemura, K.; Ikeda, N.; Shimada, Y.; Ozawa, T.
Biochem. 102, 1555-1563, 1987
Title: Molecular cloning and expression in Escherichia coli of a cDNA encoding human
Reference number: A41431; MUID:88198076; PMID:2834346
 DNA 6, 163-172, 1987
A,Title: Characterization of pancreatic elastase II cDNAs: two elastase II mRNAs are
A,Reference number: A90958; MUID:87217962; PMID:3646943
 254 -KGISRYPEKITLVHACTKRT-----ANRTKKIPPQYYTDDFAIVHLYEELTFSSNVQ 305
 306 SVCVADDETQPNDKLSLEYFGFGLNPPSD-----INQNGVDN--TGQLRYEKIEVFRSH 357
 -----KGK 411
 --TYVKGTQKL--RVGFLKPKFKDGGRGA 206
 -----RECDVKDETYD-----LLYQQCDAQ-----PGASGSGVYVRMWKRQQQKWE 333
 C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: B26823; A27432; Ā41431; S34491
K;Kawashina, I.; Tani, T.; Shimoda, K.; Takiguchi, Y.
 202 HILIATHCFAGONRDGSWNLIEDTFDRSNCKDDDYVITNOEFLKRVEFLSNK-----
 A;Molecule type: mRNA
A;Residues: 1-201,'V',203-269 <SHI>
A;Residues: 1-201,'V',203-269 <SHI>
A;Cross-references: GB:D00236; NID:g219619; PIDN:BAA00165.1; PID:g219620
A;Note: the authors translated the codon GTG for residue 202 as Cys
R;Moulard, M.; Michon, T.; Kerfelec, B.; Chapus, C.
FEBS Lett. 261, 179-183, 1990
 ----KKPHKR----KFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY---
 358 PMEIYFFQARDITDKTVACVVSLKILILNKTQASLNISLKGDSGGGAIADV-
 C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-28/Domain: propeptide #status predicted <PRO>
F;29-269/Product: pancreatic elastase IIA #status predicted <MAT>
F;29-260/Domain: trypsin homology <TRY>
F;73,121,216/Active site: His, Asp, Ser #status predicted
 334 RKIIGIFS-----GHQWVDMNGSPQDFNVAVRITPLKYAQIC 370
 : |||: |
| 12 KTIIGVLSQTSCQKRRGGNETMELYSSVGFYKNQI----CKYTGIC 453
 207 NDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDY---DYALLEL
 pancreatic elastase II (EC 3.4.21.71) A precursor - human
 Title: Further studies on the human pancreatic binary Reference number: S08253; MUID:90169111; PMID:2307232
 DB 2;
 5.6%; Score 115.5;
 Gene: GDB:ELA1
Cross-references: GDB:119866; OMIM:130120
 A, Map position: 12pter-12gter
 Molecule type: protein;Residues: 'X',18-50 <MOU>
 A; Molecule type: mRNA
A; Residues: 1-269 <FLE>
 Accession: S34491
 Accession: A27432
 ,Accession: B26823
 Accession: A41431
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Query Match
Best Local Similarity 23.4%
Matches 54; Conservative
 A; Reference number: $19890
 A; Molecule type: mRNA
A; Residues: 1-238 < KAL>
 A;Status: preliminary
 A;Accession: S1989]
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 A,Cross-references: EMBL:X62259; NID:g31246; EMBL:X62258; GB:S40923; NID:g31247; EMBL:X6555; GB:S40856; NID:g31251; EMBL:X62257; GB:S40859; NI A;Note: sequence extracted from NCBI backbone (NCBIN:109315, NCBIN:109317, NCBIN:109319, C;Comment: This apparently silent human homolog of pancreatic elastase I is a single-cog
 96
 probable pancreatic elastase (EC 3.4.21.36) pseudogene - human N;Alternate names: pancreatic elastase I homolog; pancreatic elastase I allele HEL1-16, C;Species: Homo sapiens (man) C;Species: 11-Aug-1995 #sequence_revision 17-Aug-1995 #text_change 14-Aug-1998
 trypsin-like proteinase (EC 3.4.21.-) 5G1 precursor - yellow fever mosquito (fragment) C,Species: Aedes aegypti (yellow fever mosquito) C,Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C,Accession: S19891
R;Kalhok, S.; Tabak, L.M.; Prosser, D.E.; Downe, A.E.R.; White, B.N.
submitted to the EMBL Data Library, February 1992
A;Description: Isolation, sequencing and characterization of 2 cDNA clones coding for
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 147 NYPFSTSVKLSTG-----CTGTLVAEKHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
 199 FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
 147 NYPFSTSVKLSTG-----CTGTLVAEKHVLTAAHCIHDGKTY--VKGTQKLRVGFLKPK 198
 199 FKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL-KKPHK 257
 -----SQNDGTE------QYVSVQKIVVHPYW---NSDNVAAGYDIALIRLAQSVTL 132
 8
 8
 SWPSQISLQYRSGGSWYHTCGGTLIRQNWVMTAAHCVDYQXTFRVVAGDHNL-----
 38; Indels 34;
 Score 115; DB 4; Length 258;
 5.5%; Score 115; DB 4; Length 267;
26.9%; Pred. No. 0.052;
tive 23; Mismatches 38; Indels
Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
A;Residues: 1-258 «KM»
A;Note: it is not known whethere the gene is expressed
F:19-251/Domain: trypsin homology «TRY»
 A;Map position: 12
C;Keywords: hydrolase; pseudogene; serine proteinase
 Pred. No. 0.05;
 23; Mismatches
 unctional protein in some other tissue
 Best Local Similarity 26.9%;
Matches 35; Conservative 23
 ----SONDGTE---
 Conservative
 ::::| |
124 NSYVQLGVLP 133
 258 RKFMKIGVSP 267
 258 RKFMKIGVSP 267
 133 NSYVOLGVLP 142
 A; Molecule type: DNA
A; Residues: 1-267 < KAW>
 Query Match
Best Local Similarity
Matches 35; Conserv
 A; Accession: A56615
 A;Gene: GDB:ELA1
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 90
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A; Molecule type: DNA
A; Residues: 1-285 <KUR>
A; Cross-references: UNIPROT:097SH5; GB:AE005672; PIDN:AAK74556.1; PID:g14971860; GSPDB:G?
A; Experimental source: strain TIGR4
A; Genetics:
 S.; Heide
 C;Species: Streptococcus preumoniae
C;Species: Streptococcus preumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95045
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
snon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Reference number: A95000; MUID:21357209; PMID:11463916
A)Cross-references: UNIPROT:P29787; EMBL:X64363; NID:g5563; PIDN:CMA45715.1; PID:g5564 C; Superfamily: trypsin, trypsin homology C; Keywords: hydrolase; insect midqut; protein digestion; serine proteinase F;1-11/Domain: signal sequence and propeptide (fragment) #status predicted <81G> F;12-238/Product: trypsin-like proteinase 5G1 #status predicted <MAT> F;12-238/Product: trypsin-like proteinase 5G1 #status predicted <MAT> F;12-238/Pomain: trypsin homology <fra>Frys
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 218 KFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRI
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 QQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLD 379
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us-09-658-677-18.rpr

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C;Accession: A00960; A20534
R;MacDonald, R.J.; Swift, G.H.; Quinto, C.; Swain, W.; Pictet, R.L.; Nikovits, W.; Rutter
Biochemistry, 21, 1453-1463, 1982
A;Fitle: Primary structure of two distinct rat pancreatic preproelastases determined by & A;Reference number: A00960; MUID:82182967; PMID:6918221
 RiShiragu, Y.; Yoshida, H.; Mikayama, T.; Matsuki, S.; Tanaka, J.I.; Ikenaga, H. Biochem. 99, 1707-1712, 1986
A;Title: Isolation and expression in Escherichia coli of a cDNA clone encoding porcine payReference number: A92005; WUID:86304235; PMID:3528137
 A;Molecule type: mRNA
A;Residues: 1-266 SBH:
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A;Cross-references: UNIRROT:Poorte H.; Ohmine, T.; Takiguchi, Y.
B;Tani, T.; Kawashima, I.; Furukawa, H.; Ohmine, T.; Takiguchi, Y.
A;Tatle: Characterization of a silent gene for human pancreatic elastase I: structure of
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A; Note: the authors translated the codon GGG for residue 58 as Gln, GGC for residue 126
R; Shotton, D.M.; Hartley, B.S.
Biochem. J. 131, 643-675, 1973
A; Title: Evidence for the amino acid sequence of porcine pancreatic elastase.
A; Reference number: A90267; MUID: 73229121; PMID: 4578945
 A,Crose-references: UNIPROT:P00773; GB:V01234; NID:g56088; PIDN:CAA24544.1; PID:g56089
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 Biochemietry 22, 3763-3770, 1983
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R; Shocton, D.M.; Harley, B.S.
Nature 225, 811-816, 1970
A; Title: Three-dimensional structure of tosyl-elastase.
C; Accession: JS0013; A26777; A10061; A00959
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 A; Accession: A10061
 A; Accession: A00960
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C;Species: Homo sapiens (man)
C;Date: 28-Aug-19195 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40197; A00936; A60571; S66645
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.; A; Blod. (Chem. 267, 9212, 1992
A;Title: Human adipsin is identical to complement factor D and is expressed at high leve A;Reference number: A40197; MUD:92250520; PMID:1374388
A;Accession: A40197
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R$Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FBB. Lett. 37, 300-302, 1995
A;Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement
A;Reference number: S66645, MUID:96013156; PMID:7556615
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Wolecule: 19-44,'C',46-48 <BAL>
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 Mol. Immunol. 27, 637-644, 1990
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A,Reference number: A60571; MUID:90370044; PMID:2395435
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A;Rote: a few residues were assigned from the previously published sequence of Reid et A;Note: a few residues were assigned from the previously published sequence of Reid et R;Miyata, T:; Oda, O:; Inagi, R:; Sugiyama, S:; Miyama, A.; Maeda, K.; Nakashima, I.; YMI I Immunol. 27, 637-644, 1990
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R;Niemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.B.
Biochemistry 33, 2482-2486, 1984
A;Title: Amino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
 204 RGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKI 263
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 Accession: S66645
 44;
 A; Gene: GDB: DF
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Best Local S
Matches 44
 Genetics:
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staphylococ
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bacillus ce
bacillus su
mus musculu
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GenCore version 5.1.6
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001 HL5

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005 BDR41

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006 BDR41

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| 6.0 1322 2 Q9NJSS<br>6.0 266 2 Q46644<br>6.0 266 2 Q9G491<br>5.9 339 2 Q9G891<br>5.9 541 2 Q9GX85<br>5.9 643 2 Q9GX84<br>5.9 643 2 Q9GX84<br>5.9 259 2 Q9XY61<br>5.9 449 2 Q9WF9<br>5.9 449 2 Q9WF9<br>5.8 1059 2 Q9WF9                              | ALIGNMENTS STANDARD; PRT; 383 AA. | 095084; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Serine protease 23 precursor (EC 3.4.21) (Pr Sci013) (UNQ270/PR0307). Name=PRSS23; Synonyms=ZSIG13; Homo sapiens (Human). Mamealia; Eutheria; Primates; Catarrhini; Homi | Vb;<br>N.A.<br>cal vein;<br>T.F.;<br>ne protease from human umbilical<br>L-1997) to the EMBL/GenBank/DDBJ                          | ROM N.A.<br>., Blumberg H., Jelinek L., Foster I<br>(OCT-1999) to the EMBL/GenBank/DDBJ | PubMed=112301<br>B., Wellenreut<br>B., Wellenreut<br>rhoeft A., Bey<br>nwaelder B., C<br>B., Klein M.,<br>g of human ger<br>ovel complete<br>2-435(2001).                    | MEDLINE-22887296; PubMed=12975309; DOI=10.11 Clark H.P., Gurney A.L., Abaya E., Baker K., Chen J., Chow B., Chui C., Crowley C., Curre Eaton D., Poster J., Grimaldi C., Gu Q., Has Huang A., Kim H.S., Klimowski L., Jin Y., Jo Lewis L., Liao D., Mark M., Robbie E., Sanch Seshagiri S., Simmons L., Singh J., Smith V. Vandlen R., Watanabe C., Wieand D., Woods K. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Ggodowski P., Gray A.; "The secreted protein discovery initiative (effort to identify novel human secreted and bioinformatics assessment."; Genome Res. 13:2265-2270(2003). |
| 32 124.5<br>34 124.5<br>34 123.5<br>36 123.5<br>37 123.5<br>37 123.5<br>40 122<br>41 122<br>43 1212<br>44 122<br>44 121<br>45 121                                                                                                                    | SULT 1<br>23 HUMAN<br>PS23 HUMAN  | 095084;<br>28-FEB-2003 (<br>28-FEB-2003 (<br>25-OCT-2004 (<br>Serine protea<br>ZSIG13) (UNQ2<br>Name=PRSS23;<br>HOMO sapiens<br>Eukaryota; Me                                                                                                                                                             | NCB1 Tax1D=9006;  (1) SEQUENCE FROM N.A. TISSUB—Umbilical vei Li X., Tedder T.F.; "A novel serine procells."; Submitted (JUL-1997) | UENCE F<br>ppard P                                                                      | SEQUENCE FROM N.A TISSUE=Uterus; MEDLINE=21154917; Wiemann S., Weil Ansorge W., Boech Lauber J., Dueste Mewes HW., Otte Wambutt R., Korn "Towards a catalo analysis of 500 n | MEDLINE=22887<br>Clark H.F., G<br>Clark H.F., G<br>Chen J., Chow<br>Eaton D., Fos<br>Huang A., Kim<br>Lewis L., Lia<br>Seshagiri S.,<br>Vandlen R., W<br>Yi S., Yu G.,<br>Godowski P.,<br>"The secreted<br>effort to ide<br>effort to ide<br>beiniformatic<br>Genome Res. I.                                                                                                                                                                                                                                                                                                                   |
|                                                                                                                                                                                                                                                      | RES<br>PS2<br>ID                  | AC DE                                                                                                                                                                                                                                                                 | X R R R R R R R R R R R R R R R R R R R                                                                                            | R RA                                                                                    | 8                                                                                                                                                                            | 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

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FT GHAIN 24 383 Serine protease 23.
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FT ACT SITE 240 240 Charge relay system (By similarity).
FT ACT SITE 16 316 Charge relay system (By similarity).
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MEROPS; S01.309; --
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 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.

-1 - SIMILARITY: Belongs to peptidase family Sl.

EMBL; BC079179; AAH79179.1; -.

GO; GO:0007834; C:nucleoseme; IEA.

GO; GO:0004263; F:chymotrrypain activity; IEA.

GO; GO:0004263; F:chymotrrypain activity; IEA.

GO; GO:0004263; F:chymotrrypain activity; IEA.

GO; GO:0006701; P:chromoseme organization and biogenesis (sen. . .; IEA.

GO; GO:000508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001951; Histone H4.

InterPro; IPR001254; Peptidase_Sl.
 181 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
KTYVKGTOKLRVGFLKPKFKDGGRGANDSTSAMPEOMKFOWIRVKRTHVPKGWIKGNAND
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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TISSUE=Breast
 Hydrolase;
SIGNAL
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DISULFID
 CHAIN
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 180
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 240
 301 TYDLLYQQCDAQPGASGSGVYVRWMKRPQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 61 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSNGEGRARSRDSEA 120
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 300
 301 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 9
 9
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SERAIN-25784/631, TISSUB-Tongue;

MEDLINE-25784/631, PubMed=1246681; DOI=10.1038/nature01266;

MEDLINE-25784/631, PubMed=1246681; DOI=10.1038/nature01266;

Maid of I., Osanto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Anikaido I., Osanto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Anikaid K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Minapin A., Matsuda H., Batalov S., Beisel R.W., An Balda E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., An Gasterlind T., Gariboldi M., Gissi C., Godzik A., Gough J., Antonadaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., Mockenzie L., Miki H., Nawasawa Y., Kodzierski R., King B.L., Maglott D.R., Maltais L., Marchionni L., Mockenzie L., Miki H., Nagashima T., Numata K., Okido T., Perrea G., Pescole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 1 MAGIPGLILLLVLLCVFMQVSPYNVPWKPTWPAYRLPIVLPQSTLKLAKPDFDAKAKLE
 KTYVKGTQKLRVGFLKPKYKDGAGGDNSSSSALVEKMKFQWIRVKRTHVPKGWIKGNAND
 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 121 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinosi.
 .;
0
 DB 2; Length 383;
 InterPro; IPR009003; Pept Ser_Cys.
Pfam, PF00089; Trypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
Probom; PD0010827; Histone_H4; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Hypothetical protein; Protease, Serine protease.
SEQUENCE 383 AA; 43159 MW; 4AB12CC7B66CDFC8 CRC64;
 22; Indels
 Best Local Similarity 91.4%; Pred. No. 6.4e-153; Matches 350; Conservative 11; Mismatches 22;
 Q9D6X6; Q8VEG1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 45, Last sequence update)
Serine protease 23 precursor (EC 3.4.21.-).
 382 AA.
 91.5%; Score 1903;
 361 ITPLKYAQICYWIKGNYLDCREG 383
 361 ITPLKYAQICYWIKGNYLDCREG 383
 InterPro; IPR001314; Peptidase_S1A
 STANDARD;
 Mus musculus (Mouse)
 Name=Prss23;
 MOUSE
 241
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 Query Match
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MEDLINE=2238825' Pubbed=12477932; DOI=10.1073/pnas.242603899;
A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Alteshul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Alteshul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Alteshul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Alteshul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Alteshul S.F., Zeeberg B. Buelow K.H., Schaefer C.F., Bhat N.K.,
A Alteshul S.F., Zeeberg B. Buelow K.H., Schaefer C.F., Bhat N.K.,
A Alteshul S.F., Zeeperg B. B., Bonaldo M.F., Caraninci P., Brange C.,
B. Stapleton M., Soares M.B., Bonaldo M.F., Caraninci P., Prange C.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Mara M.A.,
Butterfield X.S.N., Mara M.
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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Weils C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yana Z., Zavolan M., Zhu Y., Zhmmer A., Carninci P., Hayateu N., A Hirozane-Kishikawa T., Konno H., Nakawa M., Sakazume N., Shiraki T., Waki K., Kowai J., Aizawa K., Arakawa T., Fukuda S., A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibate K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Ranalysis of the mouse transcriptome based on functional annotation of Co, 770 full-langth CDNAs.";
 ŏ
 (By similarity).
(By similarity).
(By similarity).
 . .) (Potential).
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the peptidase S1 Family.
 Potential.
Serine protease 23.
Charge relay system (Charge relay system
 By similarity.
N-linked (GlcNAc.
 PEAM, PRO0089; Trypein; 1.
PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SMO0020; Tryp. SPC; 1.
PROSITE; PSS0240; TRYPSIN DOM; PALSE NEG.
PROSITE; PS00134; TRYPSIN IIS; 1.
PROSITE; PS00135; TRYPSIN SER; FALSE NEG.
 protease; Signal.
 Interpro; IPR009003; Pept Ser Cya.
Interpro; IPR001254; PeptIdase SI.
Interpro; IPR001314; Peptidase SIA.
 MGD; MGI:1923703; 2310046G15Rik
 EMBL; AK009847; BAB26541.1; -. EMBL; AK078518; BAC37319.1; -. EMBL; BC018517; AAH18517.1; -. HSSP; P00746; 1DSU.
MEROPS; S01.309; -.
 tumor;
 SEQUENCE FROM N.A.
 Serine
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 Query Match
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 180
 240
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS 120
 60 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETRVGIYILSNGEGRARGRDSEA 119
 239
 241 IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWBRKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 300 TYDLLYQQCDAQPGASGSGVYVRMWKRPQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 359
 9
 59
 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Manlysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
 1 MAGIPG-LFILLVLLCVFMQVSPYTVPWKPTWPAYRLPVVLPQSTLNLAKADFDAKAKLE
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 IGMDYDYALLELKKPHKRQFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE
 1 MAGIPGLLFLLFFLLCAVGOVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 STRAIN=CS7BL/6J; TISSUE=Cecum; MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male cecum cDNA, RIKEN full-length enriched
library, clone:9130215B18 product:SERINE PROTEASE (HYPOTHETICAL 43.0
kDa PROTEIN) (PROTEASE, SERINE, 23) homolog.
 Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
N-linked (GlcNAc. .) (Potential).
M --> I (in Ref. 1; BAB26541).
; 6F09A5C80A5B2306 CRC64;
 1;
 DB 1; Length 382;
 Best Local Similarity 90.9%; Pred. No. 1.1e-151; Matches 348; Conservative 14; Mismatches 20; Indels
 STRAIN=C57BL/63; TISSUE=Cecum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
 382 AA.
 90.8%; Score 1888.5; 90.9%; Pred. No. 1.1e
 361 ITPLKYAQICYWIKGNYLDCREG 383
 PRT;
 STRAIN=C57BL/6J; TISSUE=Cecum;
 206 206 N
260 260 M
382 AA; 43071 MW;
 PRELIMINARY;
 (Mouse)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Mus musculus
 CARBOHYD
 121
 181
 180
 240
 301
 SEQUENCE
 Query Match
 Q8BZS4
 RESULT 4
 Q8BZS4
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RESTANCENCE FROW N.A.

REACHAILS FROW N.A.

REACH J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rudda S., Purnon M., Hanagaki T., Haracka T., Hirozane T., Haryashida K., Purnon M., Hanagaki T., Hirozane T., Hayashida K., Purnon M., Hiracka T., Hirozane T., Rach H., Kawai J., Kojima Y., Konno H., Konno H., Konno H., Koya S., Rach H., Kawai J., Kojima Y., Konno M., Konno H., Koya S., Rach H., Rawai T., Myazaki A., Murata M., Nakamura M., Roya S., Ruihara C., Matsuyama T., Myazaki R., Murata M., Sano H., Rasato R., Salto R., Salto R., Salto R., Salto R., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Bayashizaki Y.; Tamaru A., Toya T., Yasumishi A., Muramatsu M., Hayashizaki Y.; Tamaru A., Toya T., Yasumishi A., Muramatsu M., Hayashizaki Y.; Tamaru A., Toya T., Yasumishi A., Muramatsu M., Hayashizaki Y.; Takahi A., Submitted (JUL-2001) to the EmBL/GenBank/DDBJ databases.

C. -- SIMILARITY: Belongs to peptidase family Sl.

BML, AKO33671; BARZ64201; --

BR MBL, ROO1254; Peptidase St.,

BR KO, GO:0006508; P:proteolysis and peptidolysis; IEA.

BR RINTS; PR00122; CHYMOTRYPSIN BR RINTS; PR00120; Tryp SPC: 1.

BR RINTS; PR00120; Tryp SPC: 1.

RW PROSITE; PS00134; Tryp SPC: 1.
 120
 240
 239
 59
 9
SEQUENCE FROM N.A.
STRAIN=C57BL/G0; TISSUE=Cecum;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mornalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 [5]

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN—CS7BL/6J; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Ishi Y., Nakamura S., Hazama M., Nishine T., Hazarada A., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Hazada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.; Rawai J., Raki Integrated sequence analysis (RISA) system=384-format Requencing pipeline with 384 multicapillary sequencer.";
 180 KTYVKGTQKLRVGFLKPKYKDGAGGDNSSSSAMPDKMKFQWIRVKRTHVPKGWIKGNAND
 1 MAGIBG-LFILLVLLCVFMQVSPYTVPWKKPTWPAYRLPVVLPQYTLNLAKADFDAKAKLE
 SGKSRRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDG
 KTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNAND
 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGS
 60 VSSSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETRVGIYILSNGEGRARGRDSEA
 1 MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLE
 Gaps
 ;
 DB 2; Length 382;
 21; Indels
 90.5%; Score 1882.5; DB 2, 90.6%; Pred. No. 3.5e-151; iive 14; Mismatches 21;
 Best Local Similarity 90.68 Matches 347; Conservative
 SEQUENCE FROM N.A.
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S

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altaubner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altaubner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altachul S.F., Zoeberg B., Buetow K.H., Scheefer C.P., Bhat N.K., Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia B.D., Mullahy S.J., W. Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Chanse S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., T., Geberzation and initial analysis of more than 15,000 full-length human
296 SPIIKKMPGGMIHFSGFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLK 355
 326 KRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLDCREG 383
 356 DPDKKNWKRKIIAVYSGHQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG 413
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MEDLINE=22897265, Pubmed=12975309; DOI=10.1101/gr.1293003;

MEDLINE=22897265, Pubmed=12975309; DOI=10.1101/gr.1293003;

Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.

Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimoweki L., Jin Y., Johnson S., Lee J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R., Wacanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 effort to identify novel human secreted and transmembrane proteins:
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 "The secreted protein discovery initiative (SPDI), a large-scale
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 GO:0004263; P:chymotrypsin activity; IEA.
CO:0008233; P:peptidase activity; IEA.
GO:0004295; P:trypsin activity; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein PRSS35 (ENMLS22).
Name-PRSS35, ORFNames-UNQS22;
Homo sapiens (Human).
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 -1- SIMILARITY: Belongs to peptidase family Sl. EMBL; BC037170; AAH37170.1; -. EMBL; AX358661; AAQ89024.1; -.
 Z
 413
 PRT;
 Genome Res. 13:2265-2270(2003)
 and mouse cDNA sequences."
 bioinformatics assessment.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 TISSUE=Brain;
 Q8N3Z0;
 Q8N3Z0
 9
 RESULT
QBN3 ZO
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 1,
 TYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 360
 300 TYDLLYQCDAQPGASGSGVYVRMWKRPQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVR 359
 295
IGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDE 300
 65 CGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGI--YILSSSGDGAQHRDSGSSG 122
 62 CGIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPT-----QNITTKG 115
 116 VSVRRKRQVYGTDSRFSILDKRPLINFPPSTAVKLSTGCSGILISPQHVLTAAHCVHDGK 175
 181
 176 DYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRRBASGGDOREGTREHLRERAKGGRRRKK 235
 219 ------FQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGV 265
 266 SPPAKOLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMW 325
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 123 KS-RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGK
 236 SGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGI
 7 LLFLLFFLLCAVG--QVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSS
 182 TYVKGTQKLRVGFLKPKPKDGGR------GANDSTSAMPEQMK------
 Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 20,
 Length 413;
 Query Match 50.1%; Score 1042; DB 2; Length 4 Best Local Similarity 47.8%; Pred. No. 7.7e-80; Matches 200; Conservative 68; Mismatches 100; Indels
 Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
 Pfam; PP00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 413 AA; 47098 MW; 818D9C951BD2D6C1 CRC64;
 MENCES; SULTANT, PRSS35.
GO, GO:0004263; F:chymotrypsin activity; IEA.
GO, GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
INTERPRO; IPRO01254; Peptidase_S1.
InterPro; IPRO01254; Peptidase_S1A.
InterPro; IPRO09003; Pept_Ser_Cys.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DJ223B3.1 (Putative secreted protein ZSIG13).
Name=dJ22B3.1;
 -1- SIMILARITY: Belongs to peptidase family S1. EMBL; AL121939; CAC35071.1; -.
 413 AA
 360 ITPLKYAQICYWIKGNYLDCREG 382
 361 ITPLKYAQICYWIKGNYLDCREG 383
 PRT;
 PRELIMINARY;
 Homo sapiens (Human)
 MEROPS; S01.994; -.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 301
 Query Match
 Dunn M.;
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 116 VSVRRKRQVYGTDSRFSILDKRFLTNPPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGK 175
 -----QMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGV 265
 CGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGI--YILSSSGDGAQHRDSGSSG 122
 123 KS-RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGK 181
 236 SGRGORIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGI 295
 SPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMW 325
 176 DYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKK 235
 64
 61
 326 KRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLDCREG 383
 356 DPDKKKWWKRKIIAVYSGHQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG 413
 7 LLFLLFFLLCAVG--QVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSS
 LLWLIFF - - - TPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTV
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 50; Gaps
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone: 6030424122 product:similar to DZ223E3.1
(PUTATIVE SECRETED PROTEIN ZSIG13), full insert sequence (Protease,
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 "Functional annotation of a full-length mouse cDNA collection.";
 50.0%; Score 1041; DB 2; Length 413; 47.8%; Pred. No. 9.4e-80; ive 68; Mismatches 100; Indels 50
 PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolaes; Hypothetical protein; Protease; Serine protease.
SEQUENCE 413 AA; 47070 MW; 2D438145190305C0 CRC64;
 STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 409 AA.
Peptidase_S1.
Peptidase_S1A.
Pept_Ser_Cys.
 Created)
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 25-OCT-2004 (TrEMBLrel. 28,
 Conservative
 Nature 409:685-690(2001).
 PRELIMINARY;
 RIKEN FANTOM Consortium;
 Pfam; PF00089; Trypsin;
 InterPro; IPR001254;
InterPro; IPR001314;
 nterPro; IPR009003;
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Name=Prss35;
 Best Local Sim:
Matches 200;
 serine, 35)
 216
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The RICHARD CATALGAT TISSUE-restis.

RETAIN-CTRUCK GROWNE EXPLORATION Research Group Phase I a II Team, Analysis of the mouse transcriptome based on functional annocation of RTA TISSUE-PARTYON CONNOCTION.

RETAIN-CTRUCK GROWN A.

RECLINEAR CATALGAT TISSUE-restis.

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 LLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDG-- 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 RFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSP 352
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                                                                                                                                                                                                                                                            31 TWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLPTYEEAKQYLSYETL
                                                                                                                                                                                                                                                                          28 TWHLSRIPQVVSENTIHLASPTFQADAGVVKATVCGIECQEELPAPSLSQLEESLSYETI
                                                                                                                                                                                                                                                                                                               91 YANGSRIETQVGIYIL----SSSGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDF
                                                                                                                                                                                                                                                                                                                                                                                                                       203 -GRGA-----KFQWIRVKRTHVPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                         Query Match 48.9%; Score 1016.5; DB 2; Length 409; Best Local Similarity 49.4%; Pred. No. 1.1e-77; Matches 193; Conservative 68; Mismatches 83; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Whole;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to peptidase family Sl.
EMBL; AK031411; BAC27392.1; -.
EMBL; BC075675; AAH75675.1; -.
MGD; MGI:2444800; Pres35.
GO; GO:005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase Sl.
InterPro; IPR001314; Peptidase Sl.
InterPro; IPR001031; Peptidase Sl.
InterPro; IPR001031; Peptidse Sl.
                                                                                               Interior, IPR009003; Pept_colling Pronon Pram; PR00089; Trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPC; 1.
PR05ITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
Hydrolase; Protease; Serine protease.
Hydrolase; Protease; Serine protease.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
2gc:91804.
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NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYLDCR 381
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernen R.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Whole;
Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC074028; AAH74028.1; -.
ZFIN; ZDB-GENE-040704-55; zgc:91804.
ZG): GO:0004295; Firppsin activity; IEA.
GO: GO:0004295; Firppsin activity; IEA.
GO: GO:0004295; Firppsin activity; IEA.
InterPro; IRR001254; Peptidase Sl.
InterPro; IRR001254; Peptidase Sl.
InterPro; IRR001254; Peptidase Sl.
InterPro; IRR00103; Peptidase Sl.
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PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 418 AA; 47270 MW; AF53345CEE94F720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                               Query Match
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Adachi J., Aizawa K., Akimura T., Hara A., Hashlzune W.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashlzune W.,
Rukuda S., Furuno M., Hanaqaki T., Hara A., Hashlzune W.,
Hayashida.K., Hayatuu N., Hiramoto K., Hiraoka T., Hirozane T.,
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Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Namazaki R., Ohno M., Ohasto N., Okazaki Y.,
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Sasaki D., Shibara K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
I Submitted (JUL-2001) to the EMBL/GenBank/DbBJ databases.
I. Submitty (JUL-2001) to the EMBL/GenBank/DbBJ databases.
I. Submitanity: Belongs to peptidase family Sl.
R EMBL, AK030671; BAC27073.1; -.
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MEDLLNB=20499374; PUBMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE-Head; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hiquehizaki Y.; Hiquehizaki Y.; Melidipach Coloring."; Melidipach Coloring Carning Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Hiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Fujiwake S., Inoue K., Togawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Riki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                      enriched
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 6 days neonate head CDNA, RIKEN full-length enriched
11brary, clone:5430417J04 product:similar to DJ223E3.1 (PUTATIVE
SECRETED PROTEIN ZSIG13), full insert sequence.
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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Nature 420:563-573(2002).
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo male testis CDNA, RIKEN full-length
enriched library, clone:6030466M24 product:similar to DJ223E3.1
(PUTATIVE SECRETED PROTEIN ZSIG13), full insert sequence.
                                                                                                                                                                                                                                                                                                                               47;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                              45847 MW; ASACIC582BFD352E CRC64;
                                                                                                                                                                                                                                                                             / Match 48.6%; Score 1011.5; DB Local Similarity 49.1%; Pred. No. 2.9e-77; Nes 192; Conservative 68; Mismatches 84
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                  InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001039; Pept Ser Çys.
Pfam; PR00089; Trypain; 1.
PR.INTS; PR00722; CHYMOTRYPSIN.
SMART; SMORO20; Tryp_SPC; 1.
SMART; PS00134; TRYPSIN HIS; UNKNOWN I.
Hydrolase; Protease; Serine protease.
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GO:0005615; C:extracellular space; TAS
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199 KRRCSKRSRREAESAGGSQAHLRESTTQRPGKKSRRGPRVTQGRPSFQWTRVKSTHIPKG 258
                                                                                                                                                                                                                                                                                       319 RFCSVSEESNDLLYQYCDAEAGSTGSGIYLRLKEPGQROWKRKIVAVYSGHQWYDVHGVQ 378
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MEDLINE=930647737; PubMed=1429718;
MEDLINE=930647737; PubMed=1429718;
Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E.,
Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N.;
Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N.;
"Purification, characterization, cloning, and expression of a glutamic "Pulification, characterization, cloning, and expression of a glutamic acid-specific protease from Bacillus licheniformis ATCC 14580.";
J. Biol. Chem. 267:23782-23788(1992).
                                                                                                                                                 233 WIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVY
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MEDLINE-92155199; Pubmed=1346764;
MEDLINE-92155199; Pubmed=1346764;
Syendsen I., Breddam K.;
"Isolation and amino acid sequence of a glutamic acid specific endopeptidase from Bacillus licheniformis.";
Eur. J. Biochem. 204:165-171(1992).
-i. FUNCTION: Specific for hydrolysis of peptide bonds on the carboxy side of acidic amino acid residues, with a strong preference for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-Xaa, Glu-|-Xaa.
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PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00672; V8 HIS; 1.
PROSITE; PS00673; V8 SBR; 1.
Direct protein sequencing; Hydrolase; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus licheniformis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Glutamyl endopeptidase precursor (EC 3.4.21.19)
endopeptidase) (GSE).
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InterPro; IPR00103; Pept_Ser_Cys.
InterPro; IPR00124; Peptidase_SI
InterPro; IPR008256; Peptidase_SIB.
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                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/60; TISSUE-Testis; MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Saaaki N., Carninci P., Konno H., Akiyama J., Nakhi K., Hateunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mataminoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RKEN integrated sequence analysis (RISA). system-384-format Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease; Serine protease, 409 AA: 45736 MW; E9C9B91E6800719C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:extracellular space; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR001254; Peptidase SI.
InterPro, IPR009003; Pept Ser Cys.
                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-Testis;
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Hydrolase; Protease; Serine
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GO; GO:0005615; C:extrace.
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Best Local Similarity
Matches 191; Conserv
                                                                                                                                                                                                                                                                                                                FROM N.A
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                                                                                                                                                                                                                                                                                                                SEQUENCE
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316 AA;
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05-JUL-2004
05-JUL-2004
      Hydrolase.
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                                     SEQUENCE
                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                               63 SSCGPQCHKGTPL---PTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KAEKKSPAKAPY---SIKSVIGSDDRTRVTNTTAYPYRAIVHISSSIGSCTGWMIGPKTV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 LTAAHCIHDGKT-YVKGTQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 ATAGHCIYDTSSGSFAGTATVSPG------RNGTS----YPYGSVKSTRYFI 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 LVYRFCD---VKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKII----GIFSGH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 TQWQHSGPIAISETYKLQYAM-DTYGGQSGSPVFEQSSSRTNCSGPCSLAVHTNGVYGG- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 SSGKSRRKRQIYGYDSRFSIFGKDFLLN-----YPFSTSVKLST---GCTGTLVAEKHV
                                                                                                                                                                                                                                                                                            9.3%; Score 194; DB 1; Length 316;
24.0%; Pred. No. 4.8e-08;
ative 43; Mismatches 143; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAINWATCC 14580;
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky B.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
                                                                Glutamyl endopeptidase.
Charge relay system (By similarity).
Charge relay system (By similarity).
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Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.
Ehrenreich A., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mpr (EC 3.4.21.19) (Glutamyl Endo peptidase).
Name-mpr; ORFNames=BL01804, BLi00340;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                               33611 MW; 96D7552CB7089B09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 QWVDMNGSPQDFNVAVRITPLKYAQICYW 372
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      Potential
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25-OCT-2004 (TrEMBLrel. 28, Last ann
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                                                                                                                                                                                                                                                                                                                                                            79; Conservative
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                                                                316
141
261
142
279
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                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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PubMed=15383718;
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ACT_SITE
DISULFID
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                                                                   CHAIN
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63 SSCGPQCHKGTPL---PTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 PSGWRSGNTN----YDYGAIELSEPIGNTVGYFGYSYTTSSLVGTTVTISGYPGDKTAG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 TOWOHSGPIAISETYKLOYAM-DTYGGOSGSPVFEOSSSRTNCSGPCSLAVHTNGVYGG- 291
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                                                                                                                                                                                                                                                                    28 AQAAPSPH--TPVSSDPSY-KAETSVTYDP----NIKSDQYGLYSKAFTGTGKVNETKE
                                                                                                                                                                                                                                                                                                                                                                        120 SSGKSRRKRQIYGYDSRFSIFGKDFLLN-----YPFSTSVKLST---GCTGTLVAEKHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 LVYRFCD--VKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKII----GIFSGH
                                                                                                                                                 Gaps
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                                                                                                                                             64;
                                                                        Length 316;
                                                                 9.3%; Score 194; DB 2; Length 316
24.0%; Pred. No. 4.8e-08;
tive 43; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes (serotype 4b / strain F2365).
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
Complete proteome; Hydrolase; Protesse; Serine protesse.
SEQUENCE 450 AA; 48793 MW; 54C79A67510PAD4A CRC64;
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Nucleic Acids Res. 32:2386-2395 (2004).

GO; GO:0004299; F:trypain activity; IEA.

GO; GO:0006309; P:trypain activity; IEA.

Interpro; IPRO01254; Peptidase_31.

Interpro; IPRO03254; Peptidase_51B.

Interpro; IPRO09003; Peptidase_51B.

PETIN; PRO09003; Peptidase_51B.

PRINTS; PRO090039; V8PROTEASE.

SMART; SM00728; ChW; 3.
33611 MW; 96D7552CB7089B09 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease, putative.
OrderedLocusNames=LMOf2365_1900;
                                                                                                           Best Local Similarity 24.0%
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=265669;
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272 GDFTANLVGYPGDKPMGTMWKASCEVHAENIAPEYFQYDCDTFPGSSGSSVYAYDTKSKQ 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 KQ----LPGGR-IHFSGYDNDRPGNLVYRFCDVKDE-TYDLLYQQCDAQPGASGSGVYVR 323
        169 YGSCSATLIGPRTVLTAAHCLYSHEDKDWL--SEYLFV------PGLNGSTA---
                                                                                                                                                                        273 PGGRIHFSGYDNDRP-GNLVYRFCDVKDETYDLLYQQ--CDAQPGASGSGVYVRMWKRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., IComplete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 TGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQKLRVGF-LKPKFKDGGRGANDSTSAMPEQ
                                                              215 EQMKFQWIRVKRTHVPKGWIKGNANDIG--MDYDYALLELKKPHKRKFMKIGVSPPAKQL
                                                                                                                  213 DDAPFGAFTYESAYVLQGFIDNYQGYYGSVIPWDLGIITLKQDVGTNLGWLGYA-NYDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                    332 R------IITG---VNVAESP-DANTAVRLN----AANVQWINSLY 363
                                                                                                                                                                                                                                                                                    330 QKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNY 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L DIMA KES. 7:331-338 (2000).

R REMEL, APROM3010; BABS3084.1, -.

R GO; GO:0004253; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001314; Peptidase_S1.

R InterPro; IPR009255; Peptidase_S1.

R InterPro; IPR009035; Peptidase_S1B.

R PRINTS; PR00089; Trypsin; 1.

R PRINTS; PR000803; PSPC; Ex_Cys.

R PRINTS; PR000803; VGPRCTEASE.

R SMART; SM00020; Tryp SPC; 1.

R PROSITE; PS50040; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN LHIS; UNKNOWN 1.

R COMplete protecome; Hydrolase; Percease; Serine protease.

COMPLET 271 AA; 30385 MW; 37659307C63D0D9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glutamic acid specific endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=m116878;
Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21082930; PubMed=11214968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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01-OCT-2001
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                                                                                                                    176
                                                                                                                                                                        146
                                                                                                                                                                                                                              228
                                                                                                                                                                                                                                                                                                                                       288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 KLYTQTGNISQVTANNVFYRLDTTGGSSGSGVY-----NSKKQILAV-NAYEYLNG 283
                                                                                                                                                                                                                                                                            147 LY-GK------KDGGWAKKVTVYPGYNGT-----KAPFGTAKARKMY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 SSSGDGAQHR-DSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFST-----SVKLST 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GCTGTLVAEKHVLTAAHCI--HDGKTYVKGTQKLRVGFLKPKFKDGGRGANDSTSAMP 214
                                                                                                                                                                                                                                                                                                                                                                          128 RQIYGYDSRFSIFGKDFLLN---YPFSTS----VKLSTGCT----GTLVAEKHVLTAAHC
                                                                                                                                                                  KTIFGGD-----GRKLVTNTTQYPYSTSAYLVMEFPNGKTYIGSGQLIGEDSVLTAAHC
                                                                                                                                                                                                                        177 IHDGKTYVKGTQKLRVGFLKPKFKDGG------RGANDSTSAMPEQMKFQWIRVKRTH
                                                                                                                                                                                                                                                                                                                                     229 VPKGWIKGNANDIGMDYDYALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 NLVYRFCDVKDETYDLLYQQCDAQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21082930; PubMed=11214968; Kaneko T., Sasamoto S., Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                              Gaps
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                                                              72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Phyllobacteriaceae, Mesorhizobium.
        Length 450;
                                                           85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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SMART; SM00020; Tryp SPc; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
COMPLETE PROCEOME; HYDYCHOLAGE; Protease; Serine protease.
SEQUENCE 364 AA; 39034 MW; 13BE651270E7CDD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP003001; BAB50229.1; -.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR008256; Peptidase S1.
InterPro; IPR009031; Pept_Ser_Gys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Query Match 9.0%; Score 188; DB 2; Best Local Similarity 25.9%; Pred. No. 2.4e-07; Matches 70; Conservative 43; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.6%; Score 178.5; DB 2 27.1%; Pred. No. 1.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 TGD----NFGTRITKEKLNNIYTWAFDNNL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 NGSPQDFNVAVRITPLKYAQICYWIKGNYL 378
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01-OCT-2001 (TrEMBLrel. 18, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
Glutamyl endopeptidase (EC 3.4.21.19)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MAFF303099;
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